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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:41:19 ; Search time 11.2222 Seconds
(without alignments)
69.005 Million cell updates/sec

Title: US-09-914-239-10
Perfect score: 77
Sequence: 1 TSYVKVILHMVKISG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 146418

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/1aa/5A COMB .pep.*
2: /cgn2_6/ptodata/2/1aa/5B COMB .pep.*
3: /cgn2_6/ptodata/2/1aa/6A COMB .pep.*
4: /cgn2_6/ptodata/2/1aa/6B COMB .pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS COMB .pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1 .pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	45.5	9	1 US-08-465-167A-3	Sequence 3, Appl1
2	35	45.5	9	3 US-08-159-339A-580	Sequence 580, App
3	35	45.5	9	4 US-08-627-820-3	Sequence 3, Appl1
4	35	45.5	9	4 US-08-627-820-10	Sequence 10, Appl
5	35	45.5	10	1 US-08-465-167A-2	Sequence 2, Appl1
6	35	45.5	10	1 US-08-465-167A-42	Sequence 42, Appl
7	35	45.5	10	3 US-08-159-339A-585	Sequence 585, App
8	35	45.5	10	3 US-08-627-820-2	Sequence 2, Appl1
9	34	44.2	10	1 US-08-465-167A-17	Sequence 17, Appl
10	34	44.2	10	3 US-08-159-339A-602	Sequence 602, App
11	34	44.2	10	4 US-08-627-820-17	Sequence 17, Appl
12	33	42.9	10	1 US-08-465-167A-40	Sequence 40, Appl
13	33	42.9	10	3 US-08-667-725B-63	Sequence 63, Appl
14	33	42.9	10	3 US-09-007-748-63	Sequence 63, Appl
15	33	42.9	11	1 US-08-217-188A-49	Sequence 49, Appl
16	33	42.9	11	1 US-08-667-725B-49	Sequence 49, Appl
17	33	42.9	11	3 US-08-667-725B-49	Sequence 49, Appl
18	33	42.9	11	3 US-09-007-748-49	Sequence 49, Appl
19	30	39.0	9	1 US-08-465-167A-26	Sequence 26, Appl
20	29	37.7	9	1 US-08-217-188A-11	Sequence 11, Appl
21	29	37.7	9	1 US-08-217-188A-48	Sequence 48, Appl
22	29	37.7	9	1 US-08-687-725B-11	Sequence 11, Appl
23	29	37.7	9	1 US-08-687-725B-48	Sequence 48, Appl
24	29	37.7	9	1 US-08-465-167A-29	Sequence 29, Appl
25	29	37.7	9	1 US-08-667-725B-11	Sequence 11, Appl
26	29	37.7	9	3 US-08-667-725B-48	Sequence 48, Appl
27	29	37.7	9	3 US-09-007-748-11	Sequence 11, Appl

28	29	37.7	9	3 US-09-007-748-48	Sequence 48, Appl
29	29	37.7	10	1 US-08-217-187-5	Sequence 5, Appl1
30	29	37.7	10	1 US-08-217-188A-10	Sequence 10, Appl
31	29	37.7	10	1 US-08-217-186-10	Sequence 10, Appl
32	29	37.7	10	1 US-08-261-160A-10	Sequence 10, Appl
33	29	37.7	10	1 US-08-687-726-10	Sequence 10, Appl
34	29	37.7	10	1 US-08-465-167A-7	Sequence 7, Appl1
35	29	37.7	10	2 US-08-290-381A-10	Sequence 10, Appl
36	29	37.7	10	3 US-08-668-560-5	Sequence 5, Appl1
37	29	37.7	10	3 US-08-667-725B-10	Sequence 10, Appl
38	29	37.7	10	3 US-09-007-748-10	Sequence 10, Appl
39	29	37.7	10	4 US-09-348-797-5	Sequence 5, Appl1
40	29	37.7	10	4 US-08-197-484-92	Sequence 92, Appl
41	29	37.7	10	4 US-08-197-484-151	Sequence 151, App
42	29	37.7	10	4 US-08-627-820-7	Sequence 7, Appl1
43	29	37.7	10	4 US-09-533-499B-10	Sequence 10, Appl
44	29	37.7	10	5 PCT-US95-02121-92	Sequence 92, Appl
45	29	37.7	10	5 PCT-US95-02121-151	Sequence 151, App

ALIGNMENTS

RESULT 1
US-08-465-167A-3
Sequence 3, Application US/08465167A
Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-3
Query Match 45.5%; Score 35; DB 1; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSYVKVLH 9
 Db 1 TSYVKVLEY 9

RESULT 2

US-08-159-339A-580
 ; Sequence 580, Application US/08159339A
 ; Patent No. 6037135
 ; GENERAL INFORMATION:
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Cells, Esteban
 ; TITLE OF INVENTION: HLA Binding peptides and Their
 ; NUMBER OF SEQUENCES: 1254
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/159,339A
 ; FILING DATE: 29-NOV-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/926,666
 ; FILING DATE: 07-AUG-1992
 ; APPLICATION NUMBER: US 08/027,746
 ; FILING DATE: 05-MAR-1993
 ; APPLICATION NUMBER: US 08/103,396
 ; FILING DATE: 06-AUG-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Ellen Lauver
 ; REGISTRATION NUMBER: 32,762
 ; REFERENCE/DOCKET NUMBER: 018623-005030US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 580:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-159-339A-580

Query Match 45.5%; Score 35; DB 3; Length 9;
 Best Local Similarity 77.8%; Pred. No. 3e+05;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSYVKVLH 9
 Db 1 TSYVKVLEY 9

RESULT 3

US-08-627-820-3
 ; Sequence 3, Application US/08627820
 ; Patent No. 6464980
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.

Livingston, Brian D.
 Sette, Alessandro D.
 Sidney, John C.

TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
 COMPLETE MAGE 1 GENE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Stewart Street Tower

CITY: San Francisco

STATE: CA

COUNTRY: U.S.A.

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/627,820

FILING DATE: 02-Apr-1996

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/103,623

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-60

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

QY 1 TSYVKVLH 9
 Db 1 TSYVKVLEY 9

US-08-627-820-10
 ; Sequence 10, Application US/08627820
 ; Patent No. 6464980
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Livingston, Brian D.
 ; APPLICANT: Sette, Alessandro D.
 ; APPLICANT: Sidney, John C.

TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
 COMPLETE MAGE 1 GENE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Stewart Street Tower

CITY: San Francisco

STATE: CA

COUNTRY: U.S.A.

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-627-820-10

Query Match 45.5%; Score 35; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 0;

QY 1 TSYVKVLHH 9
1 TSYVKVLEY 9

Db 1 TSYVKVLEY 9

RESULT 5
US-08-465-167A-2
Sequence 2, Application US/08465167A
Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-2

Query Match 45.5%; Score 35; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSYVKVLHH 9
2 TSYVKVLEY 10

Db 2 TSYVKVLEY 10

RESULT 6
US-08-465-167A-42
Sequence 42, Application US/08465167A
Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-42

Query Match 45.5%; Score 35; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YVKVLHHMYK 12
1 YVKVLEVIK 10

Db 1 YVKVLEVIK 10

RESULT 7

US-08-159-339A-585
; Sequence 585, Application US/08159339A
; Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 585:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-585

Query Match 45.5%; Score 35; DB 3; Length 10;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSYVKVLHH 9
2 TSYVKVLEY 10

Db

RESULT 8
US-08-627-820-2

; Sequence 2, Application US/08627820
; Patent No. 6464980
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
COMPLETE MAGE 1 GENE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-627-820-2

Query Match 45.5%; Score 35; DB 4; Length 10;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSYVKVLHH 9
2 TSYVKVLEY 10

Db

RESULT 9
US-08-465-167A-17

; Sequence 17, Application US/08465167A
; Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/103,623
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-17

Query Match 44.2%; Score 34; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SYKVLHMY 11
Db 1 SYKVLLEYI 10

RESULT 10
US-08-159-339A-602
Sequence 602, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 602:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-602

Query Match 44.2%; Score 34; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SYKVLHMY 11
Db 1 SYKVLLEYI 10

RESULT 11
US-08-627-820-17
Sequence 17, Application US/08627820
Patent No. 6464980
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-627-820-17

Query Match 44.2%; Score 34; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SYKVLHMY 11
Db 1 SYKVLLEYI 10

RESULT 12

US-08-465-167A-40

Sequence 40, Application US/08465167A

Patent No. 5750395

GENERAL INFORMATION:

APPLICANT: Fikes, John D.

APPLICANT: Livingston, Brian D.

APPLICANT: Settle, Alessandro D.

APPLICANT: Sidney, John C.

TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL

TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,167A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/103,623

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-60-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-467-9600

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-465-167A-40

US-08-465-167A-40

Query Match 42.9%; Score 33; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVL 7

DB 4 TSYVKVL 10

RESULT 13

US-08-667-725B-63

Sequence 63, Application US/08667725B

Patent No. 6063900

GENERAL INFORMATION:

APPLICANT: Melief, Cornelis J. M.

APPLICANT: Visseren, M. J. W.

APPLICANT: Kaat; W. M.

APPLICANT: van der Bruggen, Pierre

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Tumor Rejection Antigen

TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESSES:

ADDRESS: Fulbright & Jaworski LLP

STREET: 666 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,748

FILING DATE: 15 January 1998

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6147187man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/667,725B

FILING DATE: 21 June 1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6063900man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acid residues

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-667-725B-63

US-08-667-725B-63

Query Match 42.9%; Score 33; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVL 7

DB 4 TSYVKVL 10

RESULT 14

US-09-007-748-63

Sequence 63, Application US/09007748

Patent No. 6147187

GENERAL INFORMATION:

APPLICANT: Melief, Cornelis J. M.

APPLICANT: Visseren, M. J. W.

APPLICANT: Kaat; W. M.

APPLICANT: van der Bruggen, Pierre

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Tumor Rejection Antigen

TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESSES:

ADDRESS: Fulbright & Jaworski LLP

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/007,748

FILING DATE: 15 January 1998

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6147187man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-007-748-63

Query Match 42.9%; Score 33; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVL 7
|||
4 TSYVKVL 10

RESULT 15
US-08-217-188A-49
Sequence 49, Application US/08217188A
Patent No. 5554724
GENERAL INFORMATION:
APPLICANT: Meilef, Cornelis J. M.
APPLICANT: Vissers, M. J. W.
APPLICANT: Kaat, W. M.
APPLICANT: van der Bruggen, Pierre
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Tumor Rejection Antigen
TITLE OF INVENTION: Precursor MAG-2 Derived Peptides, and Uses Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,188A
FILING DATE: 24-MARCH-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5554724man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-217-188A-49

Query Match 42.9%; Score 33; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVL 7
|||
5 TSYVKVL 11

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Job time: 11.2222 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:48:04 ; Search time 35.6667 Seconds
(without alignments)
132.025 Million cell updates/sec

Title: US-09-914-239-10
Perfect score: 77
Sequence: 1 TSYVKVLHMKISG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues
Total number of hits satisfying chosen parameters: 214407

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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5: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	77	100.0	15	16	US-10-447-161-135	Sequence 135, App
2	68	88.3	15	12	US-10-149-135-2018	Sequence 2018, App
3	58	75.3	11	12	US-10-149-135-458	Sequence 458, App
4	58	75.3	11	12	US-10-149-135-777	Sequence 777, App
5	58	75.3	11	12	US-10-149-135-1071	Sequence 1071, App
6	58	75.3	11	12	US-10-149-135-1286	Sequence 1286, App
7	55	71.4	15	12	US-10-149-135-1966	Sequence 1966, App
8	54	70.1	10	12	US-10-149-135-530	Sequence 530, App
9	54	70.1	10	12	US-10-149-135-1070	Sequence 1070, App
10	54	70.1	10	12	US-10-149-135-1664	Sequence 1664, App
11	54	70.1	10	12	US-10-149-135-1859	Sequence 1859, App
12	54	70.1	11	12	US-10-149-135-312	Sequence 312, App
13	54	70.1	11	12	US-10-149-135-673	Sequence 673, App
14	54	70.1	11	12	US-10-149-135-1014	Sequence 1014, App
15	54	70.1	15	12	US-10-149-135-2007	Sequence 2007, App

16	51	66.2	10	12	US-10-149-135-909	Sequence 909, App
17	49	63.6	9	12	US-10-149-135-457	Sequence 457, App
18	49	63.6	9	12	US-10-149-135-764	Sequence 764, App
19	49	63.6	9	12	US-10-149-135-1285	Sequence 1285, App
20	49	63.6	9	12	US-10-149-135-1475	Sequence 1475, App
21	49	63.6	9	12	US-10-149-135-1649	Sequence 1649, App
22	49	63.6	9	12	US-10-149-135-1757	Sequence 1757, App
23	49	63.6	9	12	US-10-149-135-1852	Sequence 1852, App
24	49	63.6	9	15	US-10-117-937-275	Sequence 275, App
25	49	63.6	10	12	US-10-149-135-1360	Sequence 1360, App
26	49	63.6	10	12	US-10-149-135-1527	Sequence 1527, App
27	49	63.6	10	12	US-10-149-135-1691	Sequence 1691, App
28	49	63.6	10	12	US-10-149-135-1787	Sequence 1787, App
29	49	63.6	11	12	US-10-149-135-1110	Sequence 1110, App
30	49	63.6	11	12	US-10-149-135-275	Sequence 275, App
31	49	63.6	11	12	US-10-149-135-656	Sequence 656, App
32	49	63.6	11	12	US-10-149-135-984	Sequence 984, App
33	49	63.6	11	12	US-10-149-135-1187	Sequence 1187, App
34	49	63.6	15	12	US-10-149-135-1951	Sequence 1951, App
35	48	62.3	15	12	US-10-149-135-2040	Sequence 2040, App
36	48	62.3	15	12	US-10-149-135-2420	Sequence 2420, App
37	47	61.0	9	12	US-10-149-135-370	Sequence 370, App
38	47	61.0	9	12	US-10-149-135-714	Sequence 714, App
39	47	61.0	9	12	US-10-149-135-1228	Sequence 1228, App
40	47	61.0	9	14	US-10-219-850-11	Sequence 11, App1
41	47	61.0	9	15	US-10-117-937-274	Sequence 274, App1
42	47	61.0	9	15	US-10-353-678-17	Sequence 17, App1
43	46	59.7	9	12	US-10-149-135-2149	Sequence 2149, App
44	45	58.4	8	12	US-10-149-135-456	Sequence 456, App
45	45	58.4	8	12	US-10-149-135-776	Sequence 776, App

ALIGNMENTS

```
RESULT 1
US-10-447-161-135
; Sequence 135, Application US/10447161
; Publication No. US2004002314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-135
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Query Match 100.0%; Score 77; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 4; 5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMKISG 15
DB 1 TSYVKVLHMKISG 15

RESULT 2
US-10-149-135-2018
; Sequence 2018, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2018
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-2018

Query Match 88.3%; Score 68; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 YKVLHMHVXI 15
Db 1 YKVLHMHVXI 13

RESULT 3
US-10-149-135-458
Sequence 458; Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 458
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-458

Query Match 75.3%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 YKVLHMHVXI 13
Db 1 YKVLHMHVXI 11

RESULT 4
US-10-149-135-777
Sequence 777; Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 777
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-777

Query Match 75.3%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 YKVLHMHVXI 13
Db 1 YKVLHMHVXI 11

RESULT 5
US-10-149-135-1071
Sequence 1071; Application US/10149135

Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/027,146
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1071
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1071

Query Match 75.3%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMHV 11
DB 1 TSYVKVLHMHV 11

RESULT 6
US-10-149-135-1286
Sequence 1286, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1286
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1286

Query Match 75.3%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YVKVLHMHVXI 13
DB 1 YVKVLHMHVXI 11

RESULT 7
US-10-149-135-1966
Sequence 1966, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1966
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1966

Query Match 71.4%; Score 55; DB 12; Length 15;
Best Local Similarity 76.9%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YVKVLHMHVXI 15
DB 1 YVKVLHMHVXI 13

RESULT 8

US-10-149-135-530
Sequence 530, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE OR INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 530
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-530

Query Match
Best Local Similarity 70.1%; Score 54; DB 12; Length 10;
Matches 10; Conservative 100.0%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;
Cy 3 YVKVLIHMHVX 12
Db 1 YVKVLIHMHVX 10

RESULT 9

US-10-149-135-1070
Sequence 1070, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE OR INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1070
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1070

Query Match
Best Local Similarity 70.1%; Score 54; DB 12; Length 10;
Matches 10; Conservative 100.0%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;
Cy 1 TSYVKVLIHMH 10
Db 1 TSYVKVLIHMH 10

RESULT 10
US-10-149-135-1664
Sequence 1664, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE OR INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1664
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-1664

Query Match
Best Local Similarity 70.1%; Score 54; DB 12; Length 10;
Matches 10; Conservative 100.0%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;

QY 3 YVKVLHHMYK 12
| | | | |
Db 1 YVKVLHHMYK 10

RESULT 11

US-10-149-135-1859

; Sequence 1859, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1859
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1859

Query Match 70.1%; Score 54; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YVKVLHHMYK 12
| | | | |
Db 1 YVKVLHHMYK 10

RESULT 12

US-10-149-135-312

; Sequence 312, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545

Query Match 70.1%; Score 54; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 312
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-312

Query Match 70.1%; Score 54; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHM 10
| | | | |
Db 2 TSYVKVLHHM 11

RESULT 13

US-10-149-135-673

; Sequence 673, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-673

Query Match 70.1%; Score 54; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 70.1%; Score 54; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHM 10
DB 2 TSYVKVLHHM 11

RESULT 14

US-10-149-135-1014
; Sequence 1014, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1014
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1014

Query Match 70.1%; Score 54; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHM 10
DB 2 TSYVKVLHHM 11

RESULT 15

US-10-149-135-2007
; Sequence 2007, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2007
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2007

FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2007
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2007

Query Match 70.1%; Score 54; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHM 10
DB 6 TSYVKVLHHM 15

Search completed: August 17, 2004, 18:01:59
Job time : 35.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:35:29 ; Search time 8.55556 Seconds

(without alignments)
168.647 Million cell updates/sec

Title: US-09-914-239-10

Sequence: 1 TSYVKVLMHMKISG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2522

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the chance being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	29.9	15	2 I49420	placental lactogen
2	21	27.3	7	2 PQ0663	membrane protein -
3	20	26.0	13	2 A26999	carboxylesterase (
4	20	26.0	15	2 PA0001	photosystem I iron
5	19	24.7	11	2 A14454	6-phosphofructokin
6	19	24.7	12	2 A60757	enterotoxin C-1 -
7	19	24.7	14	2 PH1311	Ig heavy chain DJ
8	19	24.7	15	2 C43334	orf3 3' to aadr -
9	18	23.4	9	2 S13889	phosphoenolpyruvat
10	18	23.4	10	2 A30823	bothropstoxin - ja
11	18	23.4	12	2 A35585	cytokinin-binding
12	18	23.4	13	2 AB0764	his operon leader
13	18	23.4	14	2 A01250	angiotensin precur
14	18	23.4	14	2 B56863	photosystem I reac
15	18	23.4	14	2 PH1327	Ig heavy chain DJ
16	18	23.4	15	2 A60834	angiotensin I prec
17	18	23.4	15	2 PA0093	ennatin synthetas
18	18	23.4	15	2 A45096	thyrotrophin-releas
19	19	22.1	10	2 S74176	glucocortikase (EC
20	17	22.1	11	2 S23373	T-cell receptor al
21	17	22.1	12	2 PH1675	Ig heavy chain V r
22	17	22.1	13	2 PH1676	Ig heavy chain V r
23	17	22.1	14	1 QMWAP	polistes mastopara
24	17	22.1	14	2 PH1577	Ig heavy chain V r
25	17	22.1	14	2 PH1705	Ig heavy chain V r
26	17	22.1	14	2 A44920	2-halobenzoate 1,2
27	17	22.1	15	2 S60341	protein kinase (EC
28	17	22.1	15	2 PA0091	methionine adenosy
29	17	22.1	15	2 S14749	3-dehydroquinase -

30	17	22.1	15	2 PC1317	large granule L4 c
31	16	20.8	6	2 A46474	Fc epsilon RIIb -
32	16	20.8	8	2 T14906	hypothetical prote
33	16	20.8	10	2 I40032	trpE protein - Bac
34	16	20.8	10	2 A90345	angiotensin precur
35	16	20.8	12	2 C49215	urease (EC 3.5.1.5
36	16	20.8	12	2 S26552	T-cell receptor be
37	16	20.8	13	2 S78519	ribosomal protein
38	16	20.8	13	2 PC1008	40K extracellular
39	16	20.8	13	2 G44644	neurotoxin-associ
40	16	20.8	13	2 PC1149	equinatoxin Ia - 8
41	16	20.8	13	2 S32473	lymadfamide 3 - g
42	16	20.8	13	2 PT0256	Ig heavy chain CRD
43	16	20.8	13	2 A59491	epithelial dog all
44	16	20.8	14	1 LFERMC	trp operon leader
45	16	20.8	14	2 S19803	ubiquitin - potato

ALIGNMENTS

RESULT 1

I49420
placental lactogen I - western wild mouse (fragment)
C/Species: Mus spretus (western wild mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C/Accession: I49420
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A/Reference number: I48934; MUID:94319082; PMID:8043949
A/Accession: I49420
A/Status: preliminary; translated from GB/EMBL/DBSJ
A/Molecule type: DNA
A/Residues: 1-15 <RES>
A/Cross-references: EMBL:U05735; NID:G497071; PIDN:AA860476.1; PID:G497072
C/Superfamily: prolactin

Query Match

Best Local Similarity 29.9%; Score 23; DB 2; Length 15;
Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YVKVL 7
|:|:|
DB 1 YIKVL 5

RESULT 2

P00663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C/Species: porcine epidemic diarrhea virus
C/Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C/Accession: P00663
R/Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A/Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic issible gastroenteritis virus.
A/Reference number: JQ2191; MUID:93389433; PMID:8397280
A/Accession: P00663
A/Molecule type: mRNA
A/Residues: 1-7

A/Cross-references: GB:I4976; NID:G311650; PIDN:CA78699.1; PID:G584083
C/Comment: This virus is coronavirus related to human coronavirus 229E.
C/Keywords: membrane protein

Query Match

Best Local Similarity 27.3%; Score 21; DB 2; Length 7;
Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLH 8
|:|:|
DB 2 KVLH 5

RESULT 3

A26999

carboxylesterase (EC 3.1.1.1), intestinal - *Caenorhabditis elegans* (fragment)
 C/Species: *Caenorhabditis elegans*
 C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 07-Feb-1997
 C/Accession: A26999

R/McNee, J.D.

Biochemistry 26, 4101-4107, 1987

A/Title: Purification and characterization of a carboxylesterase from the intestine of *C. elegans*
 A/Reference number: A26999; PMID:88000636; PMID:3551439

A/Accession: A26999

A/Molecule type: protein

A/Residues: 1-13 <MCS>

C/Keywords: carboxylic ester hydrolase; intestine

Query Match 26.0%; Score 20; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 VLHMYKISG 15
 | | | | |
 DB 4 VEHNYGKEVG 13

RESULT 4

PA0001

photosystem I iron-sulfur center protein - *Arabidopsis thaliana* (fragment)
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C/Accession: PA0001

R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A/Description: Separation and characterization of *Arabidopsis* proteins by two-dimensional gel electrophoresis

A/Reference number: PA0001
 A/Accession: PA0001
 A/Molecule type: protein
 A/Residues: 1-15 <KAM>
 A/Experimental source: stem

C/Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; photosynthesis; photosystem I

Query Match 26.0%; Score 20; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HMVKI 13
 | | | | |
 DB 2 HSVKI 6

RESULT 5

A14454

6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)
 C/Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
 C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993
 C/Accession: A14454

R/Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.
 Biochem. Soc. Trans. 7, 721-723, 1979

A/Title: The N-terminal amino acid sequence of sheep heart 6-phosphofructokinase.
 A/Reference number: A14454; PMID:80004524; PMID:157859

A/Accession: A14454

A/Molecule type: protein

A/Residues: 1-11 <FOR>

C/Keywords: glycolysis; phosphotransferase

Query Match 24.7%; Score 19; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 HMVKI 12
 | | | | |
 DB 5 HHEAK 9

RESULT 6

A60757

enterotoxin C-1 - *Staphylococcus aureus* (fragments)
 C/Species: *Staphylococcus aureus*
 C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 30-Sep-1993
 C/Accession: A60757

R/Bohach, G.A.; Handley, J.P.; Schlievert, P.M.
 Infect. Immun. 57, 23-28, 1989

A/Title: Biological and immunological properties of the carboxyl terminus of staphylococcal enterotoxin C-1
 A/Reference number: A60757; PMID:89079292; PMID:2909489

A/Accession: A60757

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <BOH>

Query Match 24.7%; Score 19; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKISG 15
 | | | | |
 DB 5 VKVTG 9

RESULT 7

PH1311

Ig heavy chain DJ region (clone C68-101) - human (fragment)
 C/Species: *Homo sapiens* (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: PH1311

R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoid leukemia
 A/Reference number: PH1302; PMID:93094761; PMID:1460419

A/Accession: PH1311

A/Molecule type: DNA

A/Residues: 1-14 <WAS>

C/Keywords: heterodimer; immunoglobulin

Query Match 24.7%; Score 19; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 4.5e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLNH 9
 | | | | |
 DB 1 RILVH 5

RESULT 8

C43334

orf33' to aadr - *Rhodospseudomonas palustris* (fragment)
 C/Species: *Rhodospseudomonas palustris*
 C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C/Accession: C43334

R/Dipensa, M.; Thomas, C.T.; Kim, M.K.; Perrotta, J.A.; Gibson, J.; Hatwood, C.S.
 J. Bacteriol. 174, 5803-5813, 1992

A/Title: Anaerobic growth of *Rhodospseudomonas palustris* on 4-hydroxybenzoate is dependent on the presence of a specific amino acid
 A/Reference number: A43334; PMID:92394882; PMID:1522059

A/Accession: C43334

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-15 <DIS>

A/Cross-references: GB:M92426; NID:G151870; PID:AAA26091.1; PID:G551951
 A/Note: sequence extracted from NCBI backbone (NCBIN:112964; NCBI:P:112967)

Query Match 24.7%; Score 19; DB 2; Length 15;
 Best Local Similarity 25.0%; Pred. No. 4.8e+03;
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 SYKVLNH 9
 | | | | |
 DB 7 AYLRARH 14

RESULT 9

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize

C/Species: Zea mays (maize)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997

C/Accession: S13889

R/Jiao, J.; Chollet, R.

Arch. Biochem. Biophys. 283, 300-305, 1990

A/Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylase

A/Reference number: S13889; PMID:9112741; PMID:2148863

A/Accession: S13889

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <JIA>

C/Keywords: carbon-carbon lyase; carboxy-lyase

Query Match
Best Local Similarity 23.4%; Score 18; DB 2; Length 9;
Pred. No. 2.6e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 HHNV 11

DB 1 HHSI 4

RESULT 10

bochroptoxin - jararacusu (fragment)

C/Species: Bothrops jararacusu (jararacusu)

C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993

C/Accession: A30823

R/Homai-Brandenburg, M.T.; Queiroz, L.S.; Santo-Neto, H.; Rodrigues-Simioni, L.; Giglio,

Toxinol 26, 615-627, 1988

A/Title: Fractionation of Bothrops jararacusu snake venom: partial chemical characteriz

A/Reference number: A30823; PMID:89020120; PMID:3176051

A/Accession: A30823

A/Molecule type: protein

A/Residues: 1-10 <HOM>

Query Match
Best Local Similarity 23.4%; Score 18; DB 2; Length 10;
Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHMV 11

DB 5 LGHMI 9

RESULT 11

cytokinin-binding factor 1 - durum wheat

C/Species: Triticum durum (durum wheat)

C/Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993

C/Accession: A35585

R/Bringer, A.C.; Cooper, G.; Stevens, A.; Hauser, C.R.; Shabnowitz, J.; Hunt, D.F.; Fox

Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988

A/Title: Characterization of a benzyladenine binding-site peptide isolated from a wheat

by mass spectrometry.

A/Reference number: A35585; PMID:88320357; PMID:3413067

A/Accession: A35585

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <BRI>

Query Match
Best Local Similarity 23.4%; Score 18; DB 2; Length 12;
Pred. No. 5.7e+03;
Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 SYKVLHM 9

DB 1 AFLQPSHH 8

RESULT 12

his operon leader peptide (imported) - Salmonella enterica subsp. enterica serovar Typhi

C/Species: Salmonella enterica subsp. enterica serovar Typhi

A/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C/Accession: AB0764

R/Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,

Th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; PMID:21534947; PMID:11677608

A/Accession: AB0764

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-13 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD02432.1; PID:gl6503299; GSPDB:GN00176

C/Genes: hsl

Query Match
Best Local Similarity 23.4%; Score 18; DB 2; Length 13;
Pred. No. 6.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YKVLHM 9

DB 4 VQPKHH 9

RESULT 13

angiotensin precursor - horse (fragment)

C/Species: Equus caballus (domestic horse)

C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 15-Sep-2003

C/Accession: A92775; A01250

R/Skeggs Jr., L.T.; Kahn, U.R.; Lentz, K.; Shumway, N.P.

J. Exp. Med. 106, 439-453, 1957

A/Reference number: A92775

A/Accession: A92775

A/Molecule type: protein

A/Residues: 1-14 <SKE>

C/Superfamily: Serpin

C/Keywords: blood pressure control; hormone; vasoconstrictor

F/1-10/Product: angiotensin I #status experimental <ANI>

F/1-8/Product: angiotensin II #status experimental <ANI>

Query Match
Best Local Similarity 23.4%; Score 18; DB 2; Length 14;
Pred. No. 6.7e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKVLHM 11

DB 4 YHPRHLIV 12

RESULT 14

photosystem I reaction center complex small chain p8aB - Synecchococcus sp. (fragment)

C/Species: Synecchococcus sp.

C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 23-Feb-1996

C/Accession: B56863

R/Hatanaka, H.; Sonoi, K.; Hirano, M.; Katoh, S.

Biochim. Biophys. Acta 1141, 45-51, 1993

A/Title: Small subunits of Photosystem I reaction center complexes from Synecchococcus elc

A/Reference number: A56863; PMID:83168774; PMID:8382079

A/Accession: B56863

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <HAT>

A;Experimental source: thylakoid membranes
A;Note: sequence extracted from NCBI backbone (NCBIP:125606)
A;Note: the species was designated as Synchococcus elongatus
C;Keywords: photosystem I; thylakoid

Query Match 23.4%; Score 18; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SYVKVL 7
| |||
Db 5 SKVKIL 10

RESULT 15

PH1327

Ig heavy chain DJ region (clone C113-105) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1327

R;Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1327

A;Molecule type: DNA

A;Residues: 1-14 <MAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.4%; Score 18; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 MKTISG 15
| : |||
Db 5 MLTISG 10

Search completed: August 17, 2004, 17:54:38
Job time : 8.55556 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:32:13 ; Search time 4.88889 Seconds
(without alignments)
159.761 Million cell updates/sec

Title: US-09-914-239-10
Perfect score: 77
Sequence: 1 TSVXVXVLMHMKISG_15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 601

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	22	28.6	9	1	BS43_SERPL
2	19	24.7	15	1	YAA3_RHOA
3	18	23.4	14	1	ANGT_HORSE
4	17	22.1	12	1	UH03_BAR
5	17	22.1	14	1	MAST_POLJA
6	17	22.1	15	1	CDN4_LITCE
7	16	20.8	10	1	ANGT_BOVIN
8	16	20.8	12	1	RR16_GINBI
9	16	20.8	13	1	NP3_LYMST
10	16	20.8	14	1	LPW_CITPR
11	16	20.8	15	1	PH2_PBRAM
12	16	20.8	15	1	PLAS_MICAE
13	15	19.5	7	1	HY7_PIG
14	15	19.5	10	1	COXA_ONCMY
15	15	19.5	10	1	FARP_MANSE
16	15	19.5	10	1	UKA6_CHLTR
17	15	19.5	14	1	CRBL_VESOR
18	15	19.5	14	1	HCVI_MESOR
19	15	19.5	14	1	MAST_VESOR
20	15	19.5	15	1	ACT_PINS
21	15	19.5	15	1	NUO8_SOLTU
22	15	19.5	15	1	PC20_BRANA
23	15	19.5	15	1	RT32_BOVIN
24	15	19.5	8	1	FUSS_FUSSO
25	14	18.2	10	1	COXQ_DRABIT
26	14	18.2	12	1	OPB3_DROVI
27	14	18.2	14	1	EFTU_CANFA
28	14	18.2	15	1	AVP2_CANFA
29	14	18.2	15	1	DIDH_PERSP
30	14	18.2	15	1	EFIA_MICRA
31	14	18.2	15	1	GFPI_CANFA
32	14	18.2	15	1	GTS_ASADI
33	14	18.2	15	1	RM12_YEAST

34	14	18.2	15	1	UC16_MAIZE	P80622 zea mays (m
35	13	16.9	9	1	MOSH_CLYJA	P19852 clypeaster
36	13	16.9	9	1	NSK1_SARBU	P41492 sarcophaga
37	13	16.9	9	1	UTAD_HUMAN	P31929 homo sapien
38	13	16.9	10	1	ESR1_SCHGA	P81012 schizaphis
39	13	16.9	10	1	LSK2_LEUMA	P09039 leucophaea
40	13	16.9	10	1	UPA5_HUMAN	P30091 homo sapien
41	13	16.9	11	1	CA21_LITCI	P82087 litorea cit
42	13	16.9	11	1	CA41_LITCI	P82091 litorea cit
43	13	16.9	11	1	CX11_CONMR	P58407 conus marmo
44	13	16.9	11	1	LSK1_LEUMA	P04428 leucophaea
45	13	16.9	11	1	LSKP_PBRAM	P36885 periplaneta

ALIGNMENTS

RESULT 1	BS43_SERPL	STANDARD;	PRT;	9 AA.
ID	BS43_SERPL			
AC	P83375;			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DE	Bacteriocin serracin P 43 kDa subunit (Fragment).			
OS	Serratia plymuthica.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Serratia.			
ON	NCBI_TaxID=82996;			
RN	[1]			
RP	SEQUENCE, AND FUNCTION.			
RC	STRAIN=J7;			
RX	MEDLINE=22293561; PubMed=12406768;			
RA	Ubrine A., Sabri A., Compere P., Jacques P., Vandenberghe I.,			
RA	Van Beuven J., Thonart P.;			
RT	"Characterization of serracin P, a phage-tail-like bacteriocin, and			
RT	its activity against <i>Erwinia amylovora</i> , the fire blight pathogen."			
RL	Appl. Environ. Microbiol. 68:5704-5710(2002).			
CC	-1- FUNCTION: Major component of a prophage tail sheath (Probable).			
CC	-1- FUNCTION: Antibacterial activity against Gram-negative bacterium			
CC	<i>E. amylovora</i> .			
CC	Antibiotic; Bacteriocin.			
KW	NON TER			
FT	SEQUENCE 9 AA; 1095 MW; 1B66D412C871B1FB CRC64;			
SO				
QY	8 HHVXK1 13	28.6%;	Score 22; DB 1; Length 9;	
	:	Best Local Similarity 50.0%;	Pred. No. 1.4e+05;	
Db	3 HHGVRV 8	Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		
RESULT 2	YAA3_RHOA	STANDARD;	PRT;	15 AA.
ID	YAA3_RHOA			
AC	Q02006;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical protein in <i>aa</i> 3'region (Fragment).			
OS	Rhodopseudomonas palustris.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Bradyrhizobiaceae; Rhodopseudomonas.			
ON	NCBI_TaxID=1076;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CGA009;			
RX	MEDLINE=92394882; PubMed=1522059;			
RA	Dispensa M., Thomas C.T., Kim M.K., Petroletta J.A., Gibson J.,			
RA	Harwood C.S.;			
RT	"Anaerobic growth of <i>Rhodopseudomonas palustris</i> on 4-hydroxybenzoate			

RT is dependent on Aadr, a member of the cyclic AMP receptor protein
 RT family of transcriptional regulators.";
 RL J. Bacteriol. 174:5803-5813(1992).

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 CC or send an email to license@1sb-sib.ch).

DR EMBL: M92426; AAA26091.1; --
 DR PIR: C43334; C43334.
 KW Hypothetical protein.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1928 MW; 149B01A548D7C202 CRC64;

Query Match 24.7%; Score 19; DB 1; Length 15;
 Best Local Similarity 25.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 SYVKVLHM 9
 DB 7 AYLRARHY 14

RESULT 3

ANGT_HORSE STANDARD; PRT; 14 AA.
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
 DE (Fragment)
 CN ACT OR SERPIN8.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxId=9796;
 RN [1]
 RP SEQUENCE.

RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate.";
 RL J. Exp. Med. 106:439-453(1957).

CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin
 CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
 CC converting enzyme) then removes a dipeptide to yield the
 CC physiologically active peptide angiotensin II, the most potent
 CC pressor substance known, which helps regulate volume and mineral
 CC balance of body fluids.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC PIR: A92775; A01250.

DR PDB; 1ER8; 1S-OCT-91.

DR INTERPRO: IPR000215; Serpin.

DR PROSITE: PS00284; SERPIN; PARTIAL.

KW Vasoconstrictor; Plasma; Serpin; 3D-structure.

FT PEPTIDE 1 10 ANGIOTENSIN I.

FT PEPTIDE 2 8 ANGIOTENSIN II.

FT NON_TER 14 14 ANGIOTENSIN III.

SQ SEQUENCE 14 AA; 1759 MW; 2B9921F8BEEFBD7 CRC64;

Query Match 23.4%; Score 18; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 3.1e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YVKVLHMV 11

DB 4 YHPRHLIV 12

RESULT 4

UH03_RAT STANDARD; PRT; 12 AA.
 AC P56572;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE.

RA STRAIN=Mistar; TISSUE=Heart;
 RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 8.3, its MW is: 28 kDa.
 FT UNSURE 2 2
 FT UNSURE 9 9
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1255 MW; 46F58D10DC33053 CRC64;

Query Match 22.1%; Score 17; DB 1; Length 12;
 Best Local Similarity 28.6%; Pred. No. 3.9e+03;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 HNMVKIS 14
 DB 3 HTKIKVA 9

RESULT 5

MAST_POLJA STANDARD; PRT; 14 AA.
 AC P01517;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Polistes mastoparan.
 OS Polistes jadvigae (Paper wasp).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Polistinae; Polistes.
 NCBI_TaxId=7457;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Venom.

RA Hirai Y., Ueno Y., Yasuhara T., Yoshida H., Nakajima T.;

RT "A new mast cell degranulating peptide, polistes mastoparan, in the
 RT venom of Polistes jadvigae.";

RL Blommed. Res. 1:185-187(1980).

CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
 CC that couple to phospholipase C.

DR PIR: A01780; OWMAPP.

KW Mast cell degranulation; Amidation.

FT MOD_RES 14 14 AMIDATION.

SQ SEQUENCE 14 AA; 1636 MW; 26472A53BFA778D8 CRC64;

Query Match 22.1%; Score 17; DB 1; Length 14;
 Best Local Similarity 22.2%; Pred. No. 4.6e+03;
 Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 KYLHMVKI 13
 DB 5 KIGQHILSV 13

```

RESULT 6
CDNA_LITCE STANDARD; PRT; 15 AA.
ID CDNA_LITCE
AC P82076;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caeridin 4.
OS Litoria caerulea (Green tree frog).
OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Pelodydidae; Litoria.
OC NCBI_Taxid=30344;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. Structures of the caeridins from
RT Litoria caerulea".
RL J. Chem. Soc. Perkin Trans. 1:573-576(1993).
CC -1- FUNCTION: Caeridins show neither neuropeptide activity nor
CC antibiolic activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
CC glands.
CC -1- MASS SPECTROMETRY: MW=1504; METHOD=FAE.
KM Amphibian defense peptide; Amidation.
FT MOD RES 15
SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFBBC5195F CRC64;

Query Match 22.1%; Score 17; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 VLHMM 10
| | |
Db 9 VLHSL 13

RESULT 7
ANGT BOVIN STANDARD; PRT; 10 AA.
ID ANGT_BOVIN
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp1]-angiotensin III)]
DE (Fragment).
GN AGT OR SERPINAB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Rumiantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RT "The amino acid sequence in a hypertensin.";
RT Biochem. J. 65:246-254(1957).
CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin
CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
CC converting enzyme) then removes a dipeptide to yield the
CC physiologically active peptide angiotensin II, the most potent
CC pressor substance known, which helps regulate volume and mineral
CC balance of body fluids.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
DR PIR; A90345; A90345.
DR PDB; 3ER5; 15-JUL-92.
DR InterPro; IPR000215; Serpin.

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DR PROSITE; PS00284; SERPIN; PARTIAL.
KM Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10
FT PEPTIDE 1 8 ANGIOTENSIN I.
FT PEPTIDE 2 8 ANGIOTENSIN II.
FT NON TER 10 ANGIOTENSIN III.
SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

Query Match 20.8%; Score 16; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YVKLH 8
| | |
Db 4 YVHPH 9

RESULT 8
RR16 GINBI STANDARD; PRT; 12 AA.
ID RR16_GINBI
AC P36207;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S16 (Fragment).
GN RPS16.
OS Ginkgo biloba (Ginkgo).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
OC NCBI_Taxid=3311;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95094313; PubMed=8001171;
RA Richard M., Tremblay C., Bellemare G.;
RT "Chloroplastic genomes of Ginkgo biloba and Chlamydomonas moewusii
RT contain a chlB gene encoding one subunit of a light-independent
RT protochlorophyllide reductase."
RL Curr. Genet. 26:159-165(1994).
CC -1- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; U01531; AAA6697.1; -.
DR HAMAP; MF_00385; -; 1.
DR InterPro; IPR000307; Ribosomal_S16.
DR PROSITE; PS00732; RIBOSOMAL_S16; 1.
KM Ribosomal protein; Chloroplast.
FT NON TER 12
SQ SEQUENCE 12 AA; 1488 MW; 6700EDAF9D033734 CRC64;

Query Match 20.8%; Score 16; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 MVKI 13
| | |
Db 1 MVKL 4

RESULT 9
NP3 LYMST STANDARD; PRT; 13 AA.
ID NP3_LYMST
AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)

```

DE Lyman-DF-amide 3.
 OS Lymanaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymanaeidae; Lymanaeidae; Lymanaea.
 OX NCBI_TaxId=6523;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 AC MEDLINE=93238777; PubMed=8477756;
 RA Johnson A.H., Rehfeld J.F.;
 RT "Lymanaeidae, a new family of neuropeptides from the pond snail,
 RT Lymanaea stagnalis. Clue to cholecystokinin immunoreactivity in
 RT invertebrates?"; 213:875-879(1993).
 RL Eur. J. Biochem. 213:875-879(1993).
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
 DR PIR; S32473; S32473.
 KW Neuropeptide; Amidation.
 FT MOD RES 13 13
 FT UNSURE 12 12
 SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;

Query Match 20.8%; Score 16; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KISG 15
 DB 4 RISG 7

RESULT 10
 ID LPW_CITR STANDARD; PRT; 14 AA.
 AC P03056;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE TTP operon leader peptide.
 GN TRPL.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxId=5546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83007061; PubMed=6749821;
 RA Blumenberg M., Yanofsky C.;
 RT "Evolutionary divergence of the Citrobacter freundii tryptophan
 RT operon regulatory region: comparison with other enteric bacteria.";
 RL J. Bacteriol. 152:57-62(1982).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPHOPHAN.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J01557; -; NOT_ANNOTATED_CDS.
 DR PIR; A03592; LPEBNC;
 KW Tryptophan biosynthesis; Leader peptide.
 SQ SEQUENCE 14 AA; 1720 MW; 5B792A473E8048E7 CRC64;

Query Match 20.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VUH 8
 DB 6 VUH 8

RESULT 11
 ID PH2_PERAM STANDARD; PRT; 15 AA.
 AC P82695;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peptide hormone 2 (Bee-Venacid 2).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxId=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Abdominal perisymphathetic organs;
 RA Predel R.;
 RL Submitted (JUL-2000) to Swiss-Prot.
 CC -1- FUNCTION: Unknown.
 KW Neuropeptide.
 SQ SEQUENCE 15 AA; 1603 MW; F353DC8B1F92B8BD CRC64;

Query Match 20.8%; Score 16; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SYVK 5
 DB 11 SYVE 14

RESULT 12
 ID PLAS_MICAE STANDARD; PRT; 15 AA.
 AC P10625;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plastoeyanin (Fragment).
 GN PETE.
 OS Microcystis aeruginosa.
 OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
 OX NCBI_TaxId=1126;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89134784; PubMed=2537099;
 RA Tan S., Ho K.-K.;
 RT "Purification of an acidic plastoeyanin from Microcystis aeruginosa.";
 RL Biochim. Biophys. Acta 973:111-117(1989).
 CC -1- FUNCTION: Participates in electron transfer between P700 and the
 CC cytochrome b6-f complex in photosystem I.
 CC -1- SIMILARITY: Contains 1 plastoeyanin-like domain.
 CC -----
 CC HANAF; MF_00566; -; 1.
 DR InterPro; IPR000923; BlueCu 1.
 DR PROSITE; PS00196; COPPER_BLTB; PARTIAL.
 KW Electron transport; Copper.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1555 MW; 32B6D4662F44F969 CRC64;

Query Match 20.8%; Score 16; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 VVSG 15
 DB 5 VVSG 9

RESULT 13
 HY7_PIG

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ID HY7 FIG STANDARD; PRT; 7 AA.
AC P0153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypochalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus."
RL Horm. Metab. Res. 13:228-232(1981).
DR PIR; A01417; NYPG7.
SQ SEQUENCE 7 AA; 957 MW; 632845B1FB5059A0 CRC64;

Query Match 19.5%; Score 15; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 LHHMWK 12
DB 2 YHSHYK 7

RESULT 14
COXA_OXCMY STANDARD; PRT; 10 AA.
ID ID COXA_OXCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout."
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535CSB1AB02C3D CRC64;

Query Match 19.5%; Score 15; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYVKV 6
DB 1 SHAKV 5

RESULT 15
FARP_MANSE

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ID FARP MANSE STANDARD; PRT; 10 AA.
AC P18523;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045350; PubMed=2235684;
RA Kingan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
RA Hildebrand U.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
RA Hunt D.F.;
RT "A new peptide in the FMRFamide family isolated from the CNS of the
RT hawkmoth, Manduca sexta."
RL Peptides 11:849-856(1990).
CC -1- FUNCTION: Increases the force of neurally evoked contractions in
CC the major power-producing flight muscles, the dorsal longitudinal
CC muscles and so is likely to play a role in sustaining or promoting
CC flight behavior patterns.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; A43977; A43977.
KW Amidation; Neuropeptide; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;

Query Match 19.5%; Score 15; DB 1; Length 10;
Best Local Similarity 28.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 VLHHMWK 12
DB 3 VVHSPFLR 9

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Search completed: August 17, 2004, 17:48:52
 Job time : 4.88889 secs

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ID 005403 PRELIMINARY; PRT; 8 AA.
 AC 005403;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE DNA for ORF's from chromosome XV (fragment)
 OS Saccharomyces cerevisiae (Baker's yeast)
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;
 RX MEDLINE=96021609; PubMed=8533473;
 RA Zumbstein E., Pearson B.W., Kalogeropoulos A., Schweizer M.;
 RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
 RT more than twice as many unknown as known open reading frames."
 RL Yeast 11:975-986(1995).
 DR EMBL; X83121; CAA58183.1; -.
 FT NON TER
 SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match
 Best Local Similarity 32.5%; Score 25; DB 3; Length 8;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 7 LHMVVKI 13
 :|:|:|:
 Db 2 IHNVVKI 8

RESULT 3

ID 062544 PRELIMINARY; PRT; 15 AA.
 AC 062544;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DE Chortonic somatomammotropin hormone 1 (Placental lactogen I) (PL-I)
 DE (Fragment).
 GN CSH1 OR PL1.
 OS Mus spretus (Western wild mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPREY/ET;
 RX MEDLINE=94319082; PubMed=8043949;
 RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maizaki Y.,
 RA Nadeau J.H.;
 RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
 RT Mamm. Genome 5:349-355(1994).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- DEVELOPMENTAL STAGE: PLACENTAL LACTOGEN I IS EXPRESSED IN MID-
 CC PREGNANCY, WHILE PLACENTAL LACTOGEN II IS EXPRESSED THROUGHOUT THE
 CC LATTER HALF OF PREGNANCY.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOMOPOLIN/PROLACTIN FAMILY.
 CC EMBL; U05735; AAB60476.1; -.
 DR PIR; I49420; I49420.
 DR MGD; MGI:97606; Cchl.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR001400; Somatotropin.
 DR Pfam; PF00103; hormone; 1.
 KW Hormone; Placenta.
 FT NON TER
 SQ SEQUENCE 15 AA; 1870 MW; 6673D0680F2FB1A9 CRC64;

Query Match
 Best Local Similarity 29.9%; Score 23; DB 11; Length 15;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 YVKVL 7
 :|:|:
 Db 1 YIKVL 5

RESULT 4

ID 026100 PRELIMINARY; PRT; 14 AA.
 AC 026100;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE Ppmsp-5 (Fragment).
 GN PPMSP-5.
 OS Pratylenchus penetrans (Root-lesion nematode).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
 NCBI_TaxID=45929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maryland isolate;
 RA Setterquist R.A., Smith G.K., Jones R., Fox G.E.;
 RT "Diagnostic Probes Targeting the Major Sperm Protein Gene may be
 RT Useful for the Molecular Identification of Nematodes."
 RL J. Nematol. 0:0-0(1996).
 DR EMBL; U57830; AAB02263.1; -.
 FT NON TER
 SQ SEQUENCE 14 AA; 1775 MW; 18EB70A35334554B CRC64;

Query Match
 Best Local Similarity 28.6%; Score 22; DB 5; Length 14;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 TSYVKVLH 8
 :|:|:|:
 Db 6 TYVMKILN 13

RESULT 5

ID 040659 PRELIMINARY; PRT; 8 AA.
 AC 040659;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE Alpha-amylase (Fragment).
 DE Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91078641; PubMed=2258052;
 RA Kumagai M.H., Shan M., Terashima M., Vrkljan Z., Whitaker J.R.,
 RA Rodriguez R.L.;
 RT "Expression and secretion of rice alpha-amylase by saccharomyces
 RT cerevisiae."
 RT Gene 94:209-216(1990).
 DR EMBL; M62916; AAA33892.1; -.
 DR Gramene; Q40659; -.
 FT NON TER
 SQ SEQUENCE 8 AA; 948 MW; EBC69444732D6D6 CRC64;

Query Match
 Best Local Similarity 27.3%; Score 21; DB 10; Length 8;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 Q9TN03 PRELIMINARY; PRT; 15 AA.
 AC Q9TN03;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Class II HLA DR5 ligand.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94164692; PubMed=8119729;
 RA Falk K., Kotzschke O., Stevanovic S., Jung G., Rammensee H.G.,
 RT "Pool sequencing of natural HLA-DR, DQ, and DP ligands reveals
 RT detailed peptide motifs, constraints of processing, and general
 RT rules."
 RL Immunogenetics 39:230-242(1994).
 KW HRC.
 SQ SEQUENCE 15 AA; 1738 MW; 5C9F3CE934481042 CRC64;

Query Match 27.3%; Score 21; DB 7; Length 15;
 Best Local Similarity 40.0%; Pred. No. 7.7e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KVLHNMVKIS 14
 : : : : :
 Db 1 EALIHQLKIN 10

RESULT 7
 P83158 PRELIMINARY; PRT; 8 AA.
 ID P83158;
 AC P83158;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa
 DE polypeptide) (PSI-C) (Fragment).
 OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apte S.K., Uhlemann E., Schmid R., Allendorf K.;
 RL Submitted (OCT-2001) to Swiss-Prot.
 CC -1- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE
 CC PHOTOSYSTEM I COMPLEX.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
 CC 'BACTERIAL-TYPE' 4Fe-4S FERREDOXINS.
 CC GO: GO:0009522; C:photosystem I; IEA.
 DR GO: GO:0015979; P:photosynthesis; IEA.
 DR InterPro: IPR001450; 4Fe4S ferredoxin.
 DR PROSITE: PS00198; 4Fe4S-FERREDOXIN; PARTIAL.
 KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 962 MW; CSBBS05322DIALF5 CRC64;

Query Match 26.0%; Score 20; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 HMVKI 13
 : : : : :
 Db 2 HTVKI 6

RESULT 8
 Q9H121

ID Q9H121 PRELIMINARY; PRT; 10 AA.
 AC Q9H121;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE D309P20.1.2 (isoform 2 of guanine nucleotide binding protein (G
 DE protein); alpha stimulating activity polypeptide 1) (Fragment).
 GN GNAS1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laird G.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL121917; CAC18783.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1095 MW; 7809E3D322C7244B CRC64;

Query Match 26.0%; Score 20; DB 4; Length 10;
 Best Local Similarity 57.1%; Pred. No. 7.7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 VLHNMVK 12
 : : : : :
 Db 1 VLENLVK 7

RESULT 9
 Q9UJ73 PRELIMINARY; PRT; 13 AA.
 ID Q9UJ73;
 AC Q9UJ73;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
 GN FBP2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20237676; PubMed=10773464;
 RA Tillmann H., Stein S., Liehr T., Bechrich K.;
 RT Structure and chromosomal localization of the human and mouse muscle
 RT fructose-1,6-bisphosphatase genes.";
 RL Gene 247:241-253(2000).
 DR EMBL; AJ238482; CAB58561.1; -.
 DR GO: GO:0042132; F:fructose-bisphosphatase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1257 MW; FDB3561B05CC5721 CRC64;

Query Match 26.0%; Score 20; DB 4; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1e+04;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 LHMVKISG 15
 : : : : :
 Db 4 LHMVIGIG 12

RESULT 10
 Q9A127 PRELIMINARY; PRT; 11 AA.
 ID Q9A127;
 AC Q9A127;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Tryp[ophan]-tRNA synthetase (Fragment).
 GN TRPS.
 OS Carsonella ruddii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
 OX NCBI_TaxID=114186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2036438; PubMed=1087784;
 RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
 BA Baumann P.;
 RT "Cospeciation of psyllids and their primary prokaryotic
 endosymbionts";
 RN Appl. Environ. Microbiol. 66:2898-2905 (2000).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21125546; PubMed=11222582;
 RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
 RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont";
 RN J. Bacteriol. 183:1853-1861 (2001).
 DR EMBL; AF211132; AKK1377.1; -.
 DR GO; GO:004812; P:RNA ligase activity; IEA.
 KW Aminoacyl-tRNA synthetase.
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1331 MW; A28C67D6533059C6 CRC64;

Query Match 24.7%; Score 19; DB 2; Length 11;
 Best Local Similarity 33.3%; Pred. No. 1.3e+04;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 YVKVLH 8
 DB 5 FIKILN 10

RESULT 11
 OXSP5 PRELIMINARY; PRT; 11 AA.
 AC OXSP5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus";
 RL Hum. Genet. 105:452-459 (1999).
 DR EMBL; AJ243277; CAB45926.1; -.
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 24.7%; Score 19; DB 6; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 KYLHMVK 12
 DB 4 RVHRSVK 11

RESULT 12
 OXSC4 PRELIMINARY; PRT; 11 AA.
 AC OXSC4;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus";
 RL Hum. Genet. 105:452-459 (1999).
 DR EMBL; AJ243278; CAB45916.1; -.
 FT NON TER 1
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 24.7%; Score 19; DB 6; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 KYLHMVK 12
 DB 4 RVHRSVK 11

RESULT 13
 O86MB2 PRELIMINARY; PRT; 15 AA.
 AC O86MB2;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Acetyl-CoA carboxylase-alpha (EC 6.4.1.2) (Fragment).
 GN ACACA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Travers M.T., Barber M.C.;
 RT "Promoter III transcripts that encode an ACC-alpha with a variant N-terminus are expressed in human tissues but are not functionally conserved in mouse and rat";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ534889; CAD59557.1; -.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 KW Alternative splicing; Ligase.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1753 MW; 56B3033C9FDE56EA CRC64;

Query Match 24.7%; Score 19; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 HMVK 12
 DB 5 HLVK 8

RESULT 14
 O98YJ3 PRELIMINARY; PRT; 15 AA.
 AC O98YJ3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Truncated pol protein (Fragment).
 GN POL.

OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=992525;
 RA Schmidt B., Walter H., Moschik G., Patz C., Werwein M., Schwingel E.,
 RA Korn K.;
 RT "Recovery of HIV-1 pol gene sequences by direct sequencing of
 RT amplification products derived from plasma samples";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF347474; AAK32551.1;
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1566 MW; 26583BDD71E6E168 CRC64;

Query Match 24.7%; Score 19; DB 15; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 VKISG 15
 DB 5 VKIGG 9

RESULT 15

ID O9UP6 PRELIMINARY; PRT; 13 AA.
 AC O9UP6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Inosine monophosphate 2 (Fragment).
 GN IMPA2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97463449; PubMed=9322233;
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
 RA Detera-Wadleigh S.D.;
 RT "A novel human myo-inositol monophosphate gene, IMP.18p, maps to a
 RT susceptibility region for bipolar disorder";
 RL Mol. Psychiatry 2:393-397(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20284187;
 RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
 RA Esterling L.E., Detera-Wadleigh S.D.;
 RT "Genomic structure and novel variants of myo-inositol monophosphate
 RT 2.";
 RT Mol. Psychiatry 5:165-171(2000).
 DR EMBL; AF025884; AAD2137.1;
 DR EMBL; AF025883; AAD2137.1; JOINED.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1345 MW; FDB5871CE26EC871 CRC64;

Query Match 24.0%; Score 18.5; DB 4; Length 13;
 Best Local Similarity 41.7%; Pred. No. 1.8e+04;
 Matches 5; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

OY 7 LH--HMKISG 15
 DB 1 LHAKHGVRIIG 12

Search completed: August 17, 2004, 17:53:18
 Job time : 29.5556 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 16:11:42 ; Search time 45.333 Seconds
(without alignments)
93.490 Million cell updates/sec

Title: US-09-914-239-10

Sequence: 1 TSYVKVLMHMKISG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	3 AAB08836	AAB08836 Amino ac
2	77	100.0	15	4 AAB31319	AAB31319 Exemplary
3	77	100.0	15	5 ABG79126	ABG79126 Human Mag
4	77	100.0	30	5 AAU85062	AAU85062 Human MAG
5	77	100.0	221	4 AAE10673	AAE10673 Human mel
6	77	100.0	221	6 ABU04432	ABU04432 Human exp
7	77	100.0	282	5 AAU98925	AAU98925 Human mel
8	77	100.0	289	7 ADC35109	ADC35109 Human bre
9	77	100.0	314	2 AAY01720	AAY01720 The MAGE-
10	77	100.0	314	3 AAB02565	AAB02565 Human MAG
11	77	100.0	314	4 AAG84515	AAG84515 MAGE3 (me
12	77	100.0	314	4 AAE06853	AAE06853 Human MAG
13	77	100.0	314	4 AAE10672	AAE10672 Human mel
14	77	100.0	314	5 AAU84815	AAU84815 Human MAG
15	77	100.0	314	6 AAE34846	AAE34846 Human MAG
16	77	100.0	314	6 ABP74197	ABP74197 Human MAG
17	77	100.0	314	6 ABU04423	ABU04423 Human exp
18	77	100.0	314	6 ABU04430	ABU04430 Human exp
19	77	100.0	314	6 ABU04420	ABU04420 Human exp
20	77	100.0	314	6 ABU04418	ABU04418 Human exp
21	77	100.0	314	6 ABU04433	ABU04433 Human exp
22	77	100.0	314	6 ABU04412	ABU04412 Human exp
23	77	100.0	314	6 ABU04417	ABU04417 Human exp
24	77	100.0	314	6 ABU04415	ABU04415 Human exp
25	77	100.0	314	6 ABU04422	ABU04422 Human exp

26	77	100.0	314	6 ABU04453	ABU04453 Human exp
27	77	100.0	314	6 ABU04414	ABU04414 Human exp
28	77	100.0	314	6 ABU04455	ABU04455 Human exp
29	77	100.0	314	6 ABU04431	ABU04431 Human exp
30	77	100.0	314	6 ABU04445	ABU04445 Human exp
31	77	100.0	314	7 ADC09575	ADC09575 MAGE-3 #S
32	77	100.0	314	7 ADC35087	ADC35087 Human bre
33	77	100.0	403	2 AAY06591	AAY06591 Haemagglu
34	77	100.0	403	6 ABU04448	ABU04448 Human exp
35	77	100.0	451	2 AAY06589	AAY06589 Lipoprote
36	77	100.0	451	6 ABU04447	ABU04447 Human exp
37	77	100.0	453	2 AAY06593	AAY06593 CLYTA-MAG
38	77	100.0	453	6 ABU04449	ABU04449 Human exp
39	77	100.0	522	5 AAM50660	AAM50660 Thioresox
40	77	100.0	3541	5 AAU85130	AAU85130 Human mel
41	71	92.2	282	5 AAU98924	AAU98924 Human mel
42	71	92.2	314	4 AAB02080	AAB02080 MAGE-12 h
43	71	92.2	314	4 AAE12997	AAE12997 Human MAG
44	68	88.3	15	4 AAG84641	AAG84641 MAGE3 DR
45	67	87.0	24	5 AAU11548	AAU11548 Human con

ALIGNMENTS

RESULT 1					
ID	AAB08836	standard; peptide; 15 AA.			
XX					
AC	AAB08836;				
DT	02-JAN-2001	(first entry)			
XX					
DE	Amino acid sequence of a MAGE-3 derived immunogenic peptide.				
XX					
KW	Melanoma associated antigen-3; MAGE-3; immunogenic peptide;				
KW	major histocompatibility complex; MHC; class II molecule; tumour;				
KW	CD4+ T cell proliferation; melanoma cell; immune response; vaccine.				
XX					
OS	Homo sapiens.				
XX					
PN	W0200052045-A2.				
XX					
PD	08-SEP-2000.				
XX					
PF	23-FEB-2000; 2000MO-EP001458.				
XX					
PR	26-FEB-1999; 99IT-MI000396.				
XX					
PA	(SANR-) FOND CENT SAN RAPHAEL DEL MONTE TABOR.				
XX					
PI	Procti MF, Dellabona P;				
XX					
DR	WPI; 2000-601867/57.				
XX					
PT	Novel melanoma associated antigen (MAGE)-3 derived immunogenic peptides				
PT	useful as vaccine for inducing immune response against tumor.				
XX					
PS	Claim 1; Page 18; 27p; English.				
XX					
CC	AAB08827-37 represent melanoma associated antigen (MAGE)-3 derived				
CC	immunogenic peptides. The peptides are capable of binding to major				
CC	histocompatibility complex (MHC) class II molecules. Stimulation with the				
CC	peptides induces proliferation of CD4+ T cells, and of their cytolytic				
CC	activity. CD4+ T cells exposed to the peptides were able to cause lysis				
CC	of melanoma cells expressing MAGE-3 and HLA-DR molecules. The peptides				
CC	are useful for inducing an immune response against tumour cells				
CC	expressing a MAGE-3 antigen. They are also useful for the preparation of				
CC	anti-tumour medicament for use as a vaccine				
XX					
SQ	Sequence 15 AA;				
Query Match	100.0%; Score 77; DB 3; Length 15;				

Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMKISG 15
DB 1 TSYVKVLHMKISG 15

RESULT 2
AAB31319
ID AAB31319 standard; peptide; 15 AA.

AC AAB31319;

DT 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours and derived from MAGE-A3.

XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;

XX MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.

XX WO200078806-A1.

XX 28-DEC-2000.

XX 14-JUN-2000; 2000WO-US016287.

XX 18-JUN-1999; 99US-00336091.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Van Snick J, Leche B, Chaux P, Boon-Falleur T, Van Der Bruggen P;

XX WPI; 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
XX are presented to the class II molecules, useful for inducing immune
XX response and treating cancers characterized by expression of MAGE-A1.
XX Disclosure; Page 32; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of
XX tumours. They can be used to enhance the immune response of vaccines
XX comprising peptides derived from human MAGE-A1 HLA (human leukocyte
XX antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
XX binding protein stimulate the activity and proliferation of CD4+ T
XX lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
XX agent for diagnosing a disorder characterized by expression of MAGE-A1.
XX The protein is used for treating a disorder characterized by expression
XX of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
XX colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
XX derived from the MAGE-A1 HLA binding protein are useful in the production
XX of anti-tumour vaccines

XX Sequence 15 AA;

Query Match 100.0%; Score 77; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMKISG 15
DB 1 TSYVKVLHMKISG 15

RESULT 3
ABG79126
ID ABG79126 standard; peptide; 15 AA.

XX AC ABG79126;
XX

DT 15-NOV-2002 (first entry)

XX Human Mage-3 class II HLA tumour-restricted antigen peptide #1.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
XX lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukemia;
XX Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
XX kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
XX ovarian cancer; pancreatic cancer; epidermis; dendritic cell;
XX tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
XX cytosolic; human.

XX Homo sapiens.

XX WO200264057-A2.

XX 22-AUG-2002.

XX 15-FEB-2002; 2002WO-US005212.

XX 15-FEB-2001; 2001US-0268687P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an
XX immune effector cell and cell penetrating peptide associated with an
XX antigen or antibody.

XX Disclosure; Page 21; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector
XX cell and a cell penetrating peptide (CPP) associated with an antigen or
XX antibody. Also included are (1) a vaccine comprising (I), CPP associated
XX with an antigen, and a pharmaceutically acceptable carrier and (2)
XX preparing a composition for a disease, by providing (I) and CPP
XX associated with an antigen for a disease, and introducing (I) and CPP
XX associated with an antigen for a disease, and introducing (I) and CPP
XX are, for example, tumour antigen derived epitopes recognised by the antigen-
XX associated CPP to (I), where antigen enters into the cell. The antigens
XX infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
XX or II. The composition is useful for enhancing immunity in an animal to a
XX disease, by administering a mature dendritic cell comprising CPP
XX associated with an antigen to disease, to the animal, such that following
XX the administration, animal is protected from disease, where the animal
XX comprises both CD4+ and CD8+ T cells. It is also useful for treating a
XX disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
XX cancer, non-Hodgkin's lymphoma, leukemia, kidney cancer, adenocarcinoma,
XX breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
XX The animal is further subjected to a cancer treatment including surgery,
XX radiation, chemotherapy or gene therapy. The administration of (I),
XX preferably dendritic cell is prior to, subsequent to or concurrent with,
XX the cancer treatment. The present sequence is a tumour antigen derived
XX epitope for inclusion in the composition of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 77; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMKISG 15
DB 1 TSYVKVLHMKISG 15

RESULT 4
AAU85062
ID AAU85062 standard; peptide; 30 AA.

XX

XX 12-JUN-2003.
 PD
 XX
 PF 15-MAY-2002; 2002US-00146473;
 XX
 PR 15-MAY-2001; 2001US-0291150P;
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Scanlan MJ, Gout I, Stockert E, Old LJ, Gure A, Chen Y;
 XX
 DR WPI; 2003-829397/77.
 N-PSDB; ADC35151.
 XX
 PT Diagnosing breast cancer in subject by obtaining biological sample from
 PT subject, contacting sample with breast cancer-associated polypeptides,
 PT determining specific binding between polypeptides and agents in sample.
 XX
 PS Example 2; SEQ ID NO 75; 173pp; English.
 XX
 CC The invention describes a method of diagnosing breast cancer in subject
 CC comprising contacting biological sample from subject with at least two
 CC different breast cancer-associated polypeptides (I) encoded by nucleic
 CC acid molecules (II) comprising sequence chosen from 42 fully defined
 CC sequences as given in specification, determining specific binding between
 CC (I) and agents in sample, where presence of the binding is diagnostic for
 CC breast cancer. The method is useful for diagnosing breast cancer in a
 CC subject. The sample is blood, lymph node fluid or breast discharge fluid.
 CC This is the amino acid sequence of a breast cancer antigen.
 CC
 SQ Sequence 299 AA;

Query Match 100.0%; Score 77; DB 7; Length 299;
 Best Local Similarity 100.0%; Pred. No. 8.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TSYVKVLHMKXISG 15
 DB 281 TSYVKVLHMKXISG 295

RESULT 9
 AAY01720
 ID AAY01720 standard; protein; 314 AA.
 AC AAY01720;
 XX
 DT 25-JUN-1999 (first entry);
 XX
 DE The MAGE-3 polypeptide.
 XX
 KW MAGE-3 tumour associated gene; human leucocyte antigen Class II;
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
 KW osteosarcoma; leukemia; carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN WO914326-A1.
 XX
 PD 25-MAR-1999.
 PD
 PF 04-SEP-1998; 98WO-US018601.
 XX
 PR 12-SEP-1997; 97US-00928615.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYVR-) UNIV VRIJE BRUSSEL.
 XX
 PI Thielemans K, Heitman C, Corthals J, Chaux P, Stroobant V;
 PI Boon-Falleur T, Van Der Bruggen P, Luiten R;
 XX
 DR WPI; 1999-244031/20.
 N-PSDB; AAX26974.

XX Isolated peptides that bind to human leucocyte antigen class II
 PT molecules.
 PT
 XX
 PS Claim 1; Page 67-68; 88pp; English.
 XX
 CC The present sequence is encoded by the MAGE-3 tumour associated gene.
 CC Peptides (AAY01721-25) that bind human leucocyte antigen (HLA) Class II
 CC molecules can be derived from the MAGE-3 protein. These peptides and
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA
 CC Class II, are used to treat MAGE-3 related diseases, particularly cancers
 CC (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).
 CC The peptides are also used to produce specific antibodies. Detection of
 CC the peptides, e.g. in binding assays, particularly with antibodies, is
 CC used for diagnosis of such diseases
 CC
 SQ Sequence 314 AA;

Query Match 100.0%; Score 77; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TSYVKVLHMKXISG 15
 DB 281 TSYVKVLHMKXISG 295

RESULT 10
 AAB02565
 ID AAB02565 standard; protein; 314 AA.
 AC AAB02565;
 XX
 DT 18-AUG-2000 (first entry)
 XX
 DE Human MAGE-A3 protein sequence.
 XX
 KW MAGE-A3; HLA class II; human leucocyte antigen; antibody; vaccine;
 KW cancer; human; tumour; tumour associated gene product.
 XX
 OS Homo sapiens.
 XX
 PN WO200020581-A1.
 XX
 PD 13-APR-2000.
 PD
 PF 15-SEP-1999; 99WO-US021230.
 XX
 PR 05-OCT-1998; 98US-00166448.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (UYVR-) UNIV VRIJE BRUSSEL.
 XX
 PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
 PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;
 PI Heitman C;
 XX
 DR WPI; 2000-317713/27.
 N-PSDB; AAA37927.
 XX
 PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
 PT tumors, are fragments of MAGE-A3 which bind to and are presented to T
 PT lymphocytes by human leucocyte antigen class II molecules.
 XX
 PS Example 6; Page 98-99; 119pp; English.
 XX
 CC The present invention relates to MAGE-A3 (tumour associated gene product)
 CC human leucocyte antigen (HLA) class II-binding peptides (see AAB02566-
 CC B02595, and AAB02633-B02637). These peptides are presented to T cells in
 CC the context of HLA class II molecules. The peptides stimulate the
 CC activity and proliferation of CD4+ T lymphocytes. The invention also
 CC includes nucleotide sequences encoding MAGE-A3 peptides (see AAA37928 and
 CC AAA37938-A37940). The peptides and nucleotide sequences can be used to

CC create antibodies against the MAGE-A3 peptides, the antibodies, peptides
CC and nucleotide sequences can be used to create a vaccine. The peptides
CC are used to diagnose or treat a disorder characterized by expression of
CC MAGE-3, particularly cancer. The methods can also be used in the
CC diagnosis of disorders associated with MAGE-3 expression. Included in the
CC invention are other human tumour antigens (see AAB82596-B02637), and PCR
CC primers used in the course of the invention (see AAB37929-A37937 and
CC AAB37941-A37942)
XX
SQ Sequence 314 AA;

Query Match 100.0%; Score 77; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVXVLMHMKISG 15
DB 281 TSYVXVLMHMKISG 295

RESULT 11

AAG84515
ID AAG84515 standard; protein; 314 AA.

XX AAG84515;

DT 10-SEP-2001 (first entry)

DE MAGE3 (melanoma antigen gene) amino acid sequence.

KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytoskeletal; immunostimulant.

XX Homo sapiens.

PN WO200142267-A1.

PD 14-JUN-2001.

PF 11-DEC-2000; 2000WO-US033545.

PR 10-DEC-1999; 99US-00458298.

PA (EPIM-) EPIMUNE INC.

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;

DR WPI; 2001-375002/39.

PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
XX
XX Disclosure; Page 15; 17pp; English.

CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II); a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3; and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725

CC represent amino acid sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 314 AA;

Query Match 100.0%; Score 77; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVXVLMHMKISG 15
DB 281 TSYVXVLMHMKISG 295

RESULT 12

AAB06853
ID AAB06853 standard; protein; 314 AA.

XX AAB06853;

DT 16-OCT-2001 (first entry)

DE Human MAGE-A3 protein.

KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
KW gene therapy; human; MAGE-A3; tumour rejection antigen; TRA.

XX Homo sapiens.

PN WO200153833-A1.

PD 26-JUL-2001.

PF 19-JAN-2001; 2001WO-US002008.

PR 20-JAN-2000; 2000US-0177242P.

PR 25-OCT-2000; 2000US-0243212P.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
PI Demotte N, Schultz E;

DR WPI; 2001-488724/53.

DR N-PSDB; AAD12993.

PT Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or HLA-B44
PT binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used in
PT diagnosis and treatment of a disorder characterized by expression of MAGE
PT -A1 or -A3.
XX
XX Claim 49; Page 95; 103pp; English.

CC The invention relates to functional variants and isolated mimetics of a
CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or
CC of a MAGE-A3 HLA-B35 binding peptide, identified by methods described in
CC the specification. MAGE genes encode tumour rejection antigens (TRAs)
CC presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE
CC antigenic peptide acts by binding to HLA molecules on tumour cells and
CC stimulating recognition of these cells and thus signalling them to the
CC immune system for destruction. The peptide when presented by HLA molecule
CC induces the activation and stimulation of CD8+ cytotoxic T lymphocytes.
CC The MAGE antigenic peptide is used to treat and diagnose disorders
CC characterized by expression of MAGE-A1 or -A3. Disorders include cancers
CC e.g. melanomas, oesophages, lung, head and neck, breast, colorectal,
CC prostate, renal, bladder, hepatocellular, papillary thyroid and gastric
CC carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian
CC tumours. The present sequence is human MAGE-A3 protein
XX
SQ Sequence 314 AA;

Query Match 100.0%; Score 77; DB 4; Length 314;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHWVKISG 15
 |||||
 DB 281 TSYVKVLHHWVKISG 295

RESULT 13

AAE10672
 ID AAE10672 standard; protein; 314 AA.

XX AAE10672;

XX 18-DEC-2001 (first entry)

XX Human melanoma associated antigen 3 (MAGE-3) protein.

XX Human, melanoma associated antigen 3; MAGE-3; neuroprotective; nootropic;

XX immunosuppressive; caspase-12 activation; cell death related disease;

XX cell death inhibitor; cancer-specific protein; Alzheimer's disease;

XX neurodegenerative disease; autoimmune disease; amyotrophy; gene therapy;

XX organ disorder.

XX Homo sapiens.

XX EPI126027-A1.

XX 22-AUG-2001.

XX 16-FEB-2001; 2001EP-00301361.

XX 18-FEB-2000; 2000JP-00041927.

XX (RIKE) RIKEN KK.

XX Morishima N, Shibata T;

XX WPI; 2001-591501/67.

XX N-PSDB; AAD18140.

XX New polypeptide for treating cell death related diseases such as

XX Alzheimer's disease, neurodegenerative diseases, autoimmune diseases,

XX amyotrophy and organ disorders comprises the recombinant cancer-specific

XX protein MAGE-3.

XX Claim 9; Fig 4; 41pp; English.

XX The present sequence is melanoma associated antigen 3 (MAGE-3) protein, a

XX cancer-specific protein from human. The present invention relates to MAGE

XX -3 protein or its truncated form which specifically bind to caspase-12 or

XX pro-caspase-12 protein and inhibit their activation. MAGE-3 sequences are

XX used as cell-death inhibitors. Therapeutic agents comprising MAGE-3

XX sequence are useful for treating cell death related diseases such as

XX Alzheimer's disease, neurodegenerative diseases, autoimmune diseases,

XX amyotrophy and organ disorders. MAGE-3 gene is useful as an agent for

XX gene therapy. The sequences of the invention are useful for preventing or

XX treating a cell death-related disease developing in tissues in the

XX nervous system, vascular system, respiratory system, digestive system,

XX lymph system, urinary system, or reproductive system

XX Sequence 314 AA;

QY Query Match 100.0%; Score 77; DB 4; Length 314;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHWVKISG 15
 |||||
 DB 281 TSYVKVLHHWVKISG 295

RESULT 14

AAU84815
 ID AAU84815 standard; protein; 314 AA.

XX AAU84815;

XX 08-MAY-2002 (first entry)

XX Human MAGE-3 consensus sequence.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;

XX viral infection; human immunodeficiency virus; melanoma;

XX bacterial infection; Salmonella; Legionella; parasitic infection;

XX Trypanosoma; Toxoplasma; Giardia.

XX Homo sapiens.

XX WO200190197-A1.

XX 29-NOV-2001.

XX 25-MAY-2001; 2001WO-AU000622.

XX 26-MAY-2000; 2000AU-00007761.

XX (AUSU) UNIV AUSTRALIAN NAT.

XX Thomson SA, Ramshaw IA;

XX WPI; 2002-147575/19.

XX New synthetic polypeptides having several different segments of at least

XX one parent polypeptide linked together differently compared to the

XX linkage in the parent polypeptide, for inducing immune response against a

XX pathogen or cancer.

XX Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising

XX several different segments of at least one parent polypeptide linked

XX together in a different relationship relative to their linkage in the

XX parent polypeptide to impede, abrogate or otherwise alter at least one

XX function associated with the parent polypeptide and for inducing an

XX immune response against a pathogen or cancer. Also included are a

XX synthetic polynucleotide encoding and a computer system for designing the

XX synthetic polypeptides. The synthetic polypeptides and polynucleotides

XX are referred to as a Savine. The synthetic polypeptide is useful for

XX modulating immune responses preferably directed against a pathogen or a

XX cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head

XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,

XX osteopagias, brain, testicle, uterus), as potentiating agents.

XX Compositions comprising the polypeptide may be used in the treatment or

XX prophylaxis against viral (such as infections caused by HIV (human

XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis

XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial

XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,

XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic

XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,

XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is

XX a consensus sequence for a parent protein used to design a savine of the

XX invention

XX Sequence 314 AA;

QY Query Match 100.0%; Score 77; DB 5; Length 314;
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHWVKISG 15
 |||||
 DB 281 TSYVKVLHHWVKISG 295

RESULT 15

AAE34846
ID AAE34846 standard; protein; 314 AA.XX
AC AAE34846;XX
DT 28-MAY-2003 (first entry)XX
DE Human MAGE-A3 protein.XX
KW Human; MAGE-A3; human leukocyte antigen; HLA; cancer; gene therapy.XX
OS Homo sapiens.XX
PN W0200295051-A2.XX
PD 28-NOV-2002.XX
PF 16-MAY-2002; 2002MO-US015475.XX
PR 18-MAY-2001; 2001US-00860840.XX
PA (LUDW-) LUDWIG INST CANCER RES.XX
PI Zhang Y, Chaux P, Boon-Falleur T, Van Der Bruggen P,XX
DR WPI; 2003-148473/14.XX
DR N-PSDB; AAD53162.XX
PT New MAGE-A3 HLA class II-binding peptide or its functional variant
PT comprising 1-10 amino acid additions, substitutions or deletions, useful
PT for diagnosing and treating a disorder characterized by expression of
PT MAGE-A3, e.g. cancer.XX
PS Claim 1; Col 71-72; 38pp; English.XX
CC The invention relates to MAGE-A3 human leukocyte antigen (HLA) class II-
CC binding peptides and nucleic acid molecules encoding such peptides.
CC Peptides, agents and methods are useful for diagnosing and treating a
CC disorder characterized by expression of MAGE-A3 e.g. cancer. They are
CC also useful in preparing a medicament for treating cancer. The invention
CC is useful in gene therapy. The present sequence is human MAGE-A3 protein
XX

SQ Sequence 314 AA;

Query Match Best Local Similarity 100.0%; Score 77; DB 6; Length 314;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHWVKISG 15
Db 281 TSYVKVLHHWVKISG 295Search completed: August 17, 2004, 17:26:17
Job time : 45.333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:26:23 / Search time 37.7778 Seconds
(without alignments)
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Perfect score: 77
Sequence: 1 TSYVKVLIHHMVKISG 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

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Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	US-10-447-161-135	Sequence 135, App
2	77	100.0	30	US-10-296-734-1318	Sequence 1318, App
3	77	100.0	155	US-10-029-386-32994	Sequence 32994, A
4	77	100.0	221	US-09-784-199-4	Sequence 4, Appl
5	77	100.0	229	US-10-146-473-75	Sequence 75, Appl
6	77	100.0	314	US-09-766-889A-55	Sequence 55, Appl
7	77	100.0	314	US-09-784-199-2	Sequence 2, Appl
8	77	100.0	314	US-09-860-840-2	Sequence 2, Appl
9	77	100.0	314	US-09-849-602-29	Sequence 29, Appl
10	77	100.0	314	US-10-149-135-2440	Sequence 2440, App
11	77	100.0	314	US-10-296-734-829	Sequence 829, App
12	77	100.0	314	US-10-146-473-53	Sequence 53, Appl
13	77	100.0	314	US-10-177-390-20	Sequence 20, Appl
14	77	100.0	314	US-10-832-2	Sequence 2, Appl
15	77	100.0	314	US-10-117-937-73	Sequence 73, Appl

16	77	100.0	314	US-10-444-683-2	Sequence 2, Appl
17	77	100.0	522	US-10-296-770-2	Sequence 2, Appl
18	77	100.0	1541	US-10-296-734-1454	Sequence 1454, App
19	71	92.2	314	US-10-444-683-44	Sequence 44, Appl
20	68	88.3	15	US-10-149-135-2018	Sequence 2018, App
21	67	87.0	24	US-10-026-066-10	Sequence 10, Appl
22	67	87.0	24	US-10-026-066-24	Sequence 24, Appl
23	64	83.1	314	US-10-149-135-2439	Sequence 2439, App
24	64	83.1	314	US-10-117-937-72	Sequence 72, Appl
25	61	79.2	30	US-10-296-734-1320	Sequence 1320, App
26	58	75.3	11	US-10-149-135-458	Sequence 458, App
27	58	75.3	11	US-10-149-135-777	Sequence 777, App
28	58	75.3	11	US-10-149-135-1071	Sequence 1071, App
29	58	75.3	11	US-10-149-135-1286	Sequence 1286, App
30	55	71.4	15	US-10-149-135-1966	Sequence 1966, App
31	54	70.1	10	US-10-149-135-530	Sequence 530, App
32	54	70.1	10	US-10-149-135-1070	Sequence 1070, App
33	54	70.1	10	US-10-149-135-1664	Sequence 1664, App
34	54	70.1	10	US-10-149-135-1859	Sequence 1859, App
35	54	70.1	11	US-10-149-135-312	Sequence 312, App
36	54	70.1	11	US-10-149-135-673	Sequence 673, App
37	54	70.1	11	US-10-149-135-1014	Sequence 1014, App
38	54	70.1	15	US-10-149-135-2007	Sequence 2007, App
39	54	70.1	232	US-09-864-761-38124	Sequence 38124, A
40	52	67.5	317	US-10-218-095-2	Sequence 2, Appl
41	52	67.5	317	US-10-157-031-52	Sequence 52, Appl
42	51	66.2	10	US-10-149-135-909	Sequence 909, App
43	51	66.2	30	US-10-296-734-1278	Sequence 1278, App
44	51	66.2	309	US-09-766-889A-2	Sequence 2, Appl
45	51	66.2	12	US-10-296-734-828	Sequence 828, App

ALIGNMENTS

RESULT 1
US-10-447-161-135
; Sequence 135, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-135

Query Match 100.0%; Score 77; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLIHHMVKISG 15
Db 1 TSYVKVLIHHMVKISG 15

RESULT 2
US-10-296-734-1318
; Sequence 1318, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramsdew, Ian A

```

; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/236,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1318
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION:
US-10-296-734-1318

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Query Match      100.0%; Score 77; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 9,4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TSYKVLHNMVKISG 15
Db      13 TSYKVLHNMVKISG 27

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RESULT 3
US-10-029-386-32994
; Sequence 32994, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICX-X2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonex Sequence Listing Engine vers. 1.1
; SEQ ID NO 32994
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF002994.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: P43357, EVALUATE 2.00e-81
US-10-029-386-32994

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Query Match      100.0%; Score 77; DB 14; Length 155;
Best Local Similarity 100.0%; Pred. No. 5,3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TSYKVLHNMVKISG 15
Db      122 TSYKVLHNMVKISG 136

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RESULT 4
US-09-784-199-4
; Sequence 4, Application US/09784199
; Patent No. US20020164738A1
; GENERAL INFORMATION:
; APPLICANT: MORISHIMA, No. US20020164738A1unlro
; APPLICANT: SHIBATA, Takehiko
; TITLE OF INVENTION: CELL DEATH INHIBITORY PROTEIN
; FILE REFERENCE: 04853-0057-00000
; CURRENT APPLICATION NUMBER: US/09/784,199
; CURRENT FILING DATE: 2001-06-21

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; PRIOR APPLICATION NUMBER: JP 2000-41927
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-199-4

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Qy      1 TSYKVLHNMVKISG 15
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RESULT 5
US-10-146-473-75
; Sequence 75, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(CRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/10/146,473
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-75

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Query Match      100.0%; Score 77; DB 14; Length 299;
Best Local Similarity 100.0%; Pred. No. 0,00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TSYKVLHNMVKISG 15
Db      281 TSYKVLHNMVKISG 295

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RESULT 6
US-09-766-889A-55
; Sequence 55, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Strobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59

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SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 55
 LENGTH: 314
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-766-889A-55

Query Match
 Best Local Similarity 100.0%; Score 77; DB 9; Length 314;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
 |||||
 DB 281 TSYVKVLHHMVKISG 295

RESULT 7
 US-09-784-199-2
 ; Sequence 2, Application US/09784199
 ; Patent No. US20020164738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MORISHIMA, No. US20020164738A1unh1ro
 ; APPLICANT: SHIBATA, Takehiko
 ; TITLE OF INVENTION: CELL DEATH INHIBITORY PROTEIN
 ; FILE REFERENCE: 04853-0057-00000
 ; CURRENT APPLICATION NUMBER: US/09/784,199
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: JP 2000-41927
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-784-199-2

Query Match
 Best Local Similarity 100.0%; Score 77; DB 9; Length 314;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
 |||||
 DB 281 TSYVKVLHHMVKISG 295

RESULT 8
 US-09-860-840-2
 ; Sequence 2, Application US/09860840
 ; Publication No. US20030049722A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Yi
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Boon, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; TITLE OF INVENTION: MAG-2/3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
 ; FILE REFERENCE: 10461/7110 (JRV)
 ; CURRENT APPLICATION NUMBER: US/09/860,840
 ; PRIOR FILING DATE: 2001-05-18
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-860-840-2

Query Match
 Best Local Similarity 100.0%; Score 77; DB 10; Length 314;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
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DB 281 TSYVKVLHHMVKISG 295

RESULT 9
 US-09-849-602-29
 ; Sequence 29, Application US/09849602
 ; Publication No. US20030165834A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Matthew J.
 ; APPLICANT: Old, Lloyd J.
 ; APPLICANT: Stockert, Elisabeth
 ; APPLICANT: Chen, Yao-Tseng
 ; TITLE OF INVENTION: Colon Cancer Antigen Panel
 ; FILE REFERENCE: 10461/7105(JRV)
 ; CURRENT APPLICATION NUMBER: US/09/849,602
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-849-602-29

Query Match
 Best Local Similarity 100.0%; Score 77; DB 10; Length 314;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
 |||||
 DB 281 TSYVKVLHHMVKISG 295

RESULT 10
 US-10-149-135-2440
 ; Sequence 2440, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esben
 ; APPLICANT: Keogh, Elisa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT APPLICATION NUMBER: US/10/149,135
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2440
 ; LENGTH: 314
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-149-135-2440

Query Match
 Best Local Similarity 100.0%; Score 77; DB 12; Length 314;

Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 TSYVKVLHHMVKISG 15
|||||
Db 281 TSYVKVLHHMVKISG 295

RESULT 11

US-10-296-734-829
; Sequence 829, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 829
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAGE-3 consensus polypeptide
US-10-296-734-829

Query Match
Best Local Similarity 100.0%; Score 77; DB 14; Length 314;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
|||||
Db 281 TSYVKVLHHMVKISG 295

RESULT 12

US-10-146-473-53
; Sequence 53, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gue, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-53

Query Match
Best Local Similarity 100.0%; Score 77; DB 14; Length 314;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
|||||
Db 281 TSYVKVLHHMVKISG 295

RESULT 13

US-10-177-390-20
; Sequence 20, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wc/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-390-20

Query Match
Best Local Similarity 100.0%; Score 77; DB 14; Length 314;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
|||||
Db 281 TSYVKVLHHMVKISG 295

RESULT 14

US-10-170-832-2
; Sequence 2, Application US/10170832
; Publication No. US2003017092A1
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Strobant, Vincent
; APPLICANT: Boon-Pallieur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-2

Query Match
Best Local Similarity 100.0%; Score 77; DB 14; Length 314;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHHMVKISG 15
|||||
Db 281 TSYVKVLHHMVKISG 295

RESULT 15

US-10-117-937-73
; Sequence 73, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMVUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.

Thu Aug 19 07:12:53 2004

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; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTL1MM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-73
    
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Query Match      100.0%; Score 77; DB 15; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    
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QY      1 TSYVKVLHMMVKISG 15
      |||||
Db      281 TSYVKVLHMMVKISG 295
    
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 Job time : 37.7778 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:09:00 ; Search time 9.1111 Seconds
(without alignments)
158.364 Million cell updates/sec

Title: US-09-914-239-10
Perfect score: 77
Sequence: 1 TSVYKVLHNMVKISG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	314	2 JC2361	melanoma antigen M
2	77	100.0	314	2 JC2360	melanoma antigen M
3	71	92.2	314	2 I54519	melanoma antigen M
4	64	83.1	314	2 I68889	melanoma antigen M
5	52	67.5	317	2 I38661	melanoma antigen M
6	42	54.5	292	2 S54533	ribosomal protein
7	42	54.5	301	2 T16067	hypothetical prote
8	42	54.5	304	2 A96642	hypothetical prote
9	42	54.5	371	2 D70357	conserved hypochet
10	39.5	51.3	361	2 H71631	queine tRNA-ribos
11	39	50.6	327	2 H83559	serine/threonine-p
12	39	50.6	704	2 A26125	heat shock protein
13	39	50.6	820	2 T41978	helicase - human h
14	39	50.6	1142	2 G89453	ubiquitin-protein
15	39	50.6	1950	2 S12332	ubiquitin-protein
16	39	50.6	373	2 B69860	conserved hypochet
17	38	49.4	379	2 G84124	acyl-CoA dehydroge
18	38	49.4	399	2 G96590	unknown protein P2
19	38	49.4	473	2 F83728	phosphoribosylpyro
20	38	49.4	618	2 E83853	hypothetical prote
21	38	49.4	671	2 JC2029	annexin - chicken
22	38	49.4	695	2 B84495	hypothetical prote
23	38	49.4	745	2 S57048	hypothetical prote
24	37	48.1	102	2 D83896	potassium channel
25	37	48.1	261	2 AC0164	probable transport
26	37	48.1	305	2 C72366	tRNA delta-2-isope
27	37	48.1	453	2 G96533	protein F12M16.27
28	37	48.1	520	2 H96546	hypothetical prote
29	37	48.1	667	2 G89978	DNA ligase (import

30	37	48.1	860	2 S64366	hypothetical prote
31	37	48.1	958	2 H84783	probable PHD-type
32	37	48.1	1100	2 G84534	probable retroelem
33	37	48.1	1205	2 A55015	bumetanide-sensiti
34	37	48.1	1212	2 A57187	bumetanide-sensiti
35	37	48.1	1212	2 T31102	filamentous hemagg
36	36	46.8	163	2 E72550	hypothetical prote
37	36	46.8	174	2 E81741	conserved hypochet
38	36	46.8	185	2 S27936	hypothetical prote
39	36	46.8	187	2 E90390	hypothetical prote
40	36	46.8	266	2 T39301	probable o-methyl
41	36	46.8	284	2 E72535	probable 4-hydroxy
42	36	46.8	315	2 I38668	melanoma antigen M
43	36	46.8	356	2 T29656	hypothetical prote
44	36	46.8	412	2 AC2152	dolichyl-phosphate
45	36	46.8	455	2 H86297	hypothetical prote

ALIGNMENTS

RESULT 1
JC2361
melanoma antigen MAGE-3 - human
N/Alternate names: MAGE 3 protein
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 18-Feb-2000
C/Accession: JC2361; PH1296; I38438
R/Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A/Title: Cloning and analysis of MAGE-1-related genes.
A/Reference number: JC2358; MUID:94311935; PMID:8037761
A/Accession: JC2361
A/Molecule type: mRNA
A/Residues: 1-314 <DIN>
A/Experimental source: melanoma cell line DM150
R/Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel, J. Exp. Med. 176, 1453-1457, 1992
A/Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A/Reference number: PH1294; MUID:93018875; PMID:1402668
A/Accession: PH1296
A/Molecule type: DNA
A/Residues: 168-176 <TRA>
R/Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De Plaet J. Exp. Med. 179, 921-930, 1994
A/Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous cy
A/Reference number: I38438; MUID:94157413; PMID:8113684
A/Accession: I38438
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-314 <RBS>
A/Cross-references: EMBL:U03735; NID:G468825; PIDN:AAA17446.1; PID:G468826
C/Genetics:
A/Gene: MAGE-3
C/Superfamily: tumor associated protein MAGE
P:168-176/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 77; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSVYKVLHNMVKISG 15
DB 281 TSVYKVLHNMVKISG 295

RESULT 2
JC2360
melanoma antigen MAGE-6 - human
N/Alternate names: tumor-associated antigen, MAGE-3b
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 18-Feb-2000
C/Accession: JC2360; PH1301; I38665; G01445

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R; Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994.
A; Title: Cloning and analysis of MAGE-1-related genes.
A; Reference number: J02358; MUID:94311935; PMID:8037761
A; Accession: J02358
A; Molecule type: mRNA
A; Residues: 1-314 <DIN>
A; Experimental source: melanoma cell line DM150
R; Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A; Title: A nonpeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A; Reference number: PH1294; MUID:93018875; PMID:1402688
A; Accession: PH1294
A; Molecule type: DNA
A; Residues: 168-176 <TRA>
R; De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Boon,
T.
Immunogenetics 40, 360-369, 1994
A; Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A; Reference number: 138659; MUID:95012457; PMID:7927540
A; Accession: 138659
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-314 <RES>
A; Cross-references: EMBL:U10691; NID:9533522; PIDN:AAA68875.1; PID:9533523
R; Fenton, R.G.
submitted to the EMBL Data Library, June 1994
A; Reference number: G07126
A; Accession: G07126
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-314 <FEN>
A; Cross-references: EMBL:U10339; NID:9499121; PIDN:AAA19006.1; PID:9499122
A; Gene: GDB:MAGEA6; MAGE6
A; Cross-references: GDB:331121
A; Map position: Xq28-Xq28
A; Introns: #status absent
C; Superfamily: tumor associated protein MAGE
F; 168-176/Region: HLA-A1 binding #status predicted

Query Match          100.0%; Score 77; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHNMVKISG 15
Db 281 TSYVKVLHNMVKISG 295

RESULT 3
154519
melanoma antigen MAGE-12 - human
N; Alternate names: MAGE 21 protein
C; Species: Homo sapiens (man)
C; Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 18-Feb-2000
C; Accession: 154519; J02362; PH1295
R; De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39, 121-129, 1994
A; Title: Sequence and expression pattern of the human MAGE2 gene.
A; Reference number: 154519; MUID:94102805; PMID:8276455
A; Accession: 154519
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-314 <DES>
A; Cross-references: GB:118877; NID:9499345; PIDN:AAA19023.1; PID:9499346
R; Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A; Title: Cloning and analysis of MAGE-1-related genes.
A; Reference number: J02358; MUID:94311935; PMID:8037761
A; Accession: J02358
A; Molecule type: mRNA
A; Residues: 1-314 <DIN>

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A; Experimental source: melanoma cell line DM150; MAGE-12F
R; Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A; Title: A nonpeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A; Reference number: PH1294; MUID:93018875; PMID:1402688
A; Accession: PH1294
A; Molecule type: DNA
A; Residues: 168-176 <TRA>
A; Experimental source: MAGE-21
A; Accession: PH1295
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 168-176 <TRA>
A; Cross-references: GDB:331129
A; Gene: GDB:MAGEA12; MAGE12; MAGE-12F
A; Map position: Xq28-Xq28
C; Superfamily: tumor associated protein MAGE
F; 168-176/Region: HLA-A1 binding #status predicted

Query Match          92.2%; Score 71; DB 2; Length 314;
Best Local Similarity 86.7%; Pred. No. 8.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHNMVKISG 15
Db 281 TSYVKVLHNMVKISG 295

RESULT 4
168889
melanoma antigen MAGE-2 - human
N; Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2
C; Species: Homo sapiens (man)
C; Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 18-Feb-2000
C; Accession: 168889; PH1294
R; De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39, 121-129, 1994
A; Title: Sequence and expression pattern of the human MAGE2 gene.
A; Reference number: 154519; MUID:94102805; PMID:8276455
A; Accession: 168889
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-314 <RES>
A; Cross-references: GB:118920; NID:9436180; PIDN:AAA17729.1; PID:9436181
R; Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A; Title: A nonpeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A; Reference number: PH1294; MUID:93018875; PMID:1402688
A; Accession: PH1294
A; Molecule type: DNA
A; Residues: 168-176 <TRA>
A; Cross-references: GDB:273684
A; Gene: GDB:MAGEA2; MAGE2
A; Cross-references: GDB:273684
A; Map position: Xq28-Xq28
C; Superfamily: tumor associated protein MAGE

Query Match          83.1%; Score 64; DB 2; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.0014;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSYVKVLHNMVKISG 15
Db 281 TSYVKVLHNMVKISG 295

RESULT 5
138661
melanoma antigen MAGE-4 - human
N; Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2
C; Species: Homo sapiens (man)
C; Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 18-Feb-2000
C; Accession: 138661; 138662; PH1297; J02359; G01446
R; De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Boon,
T.
Immunogenetics 40, 360-369, 1994
A; Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam

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A:Reference number: I36659; MUID:95012457; PMID:7927540
A:Accession: I36661
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-317 <DEP1>
A:Cross-references: EMBL:U10687; NID:G533514; PIDN:AAA68871.1; PID:G533515
A:Experimental source: antigen MAGE-4a
A:Accession: I38662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-172, 'T', 174-317 <DEP2>
A:Cross-references: EMBL:U10688; NID:G533516; PIDN:AAA68872.1; PID:G533517
A:Experimental source: antigen MAGE-4b
R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
  J. Exp. Med. 176, 1453-1457, 1992
A:Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A:Reference number: PH1294; MUID:93018875; PMID:1402688
A:Accession: PH1297
A:Molecule type: DNA
A:Residues: 169-177 <TRAI>
A:Experimental source: antigen MAGE-4
A:Accession: PH1298
A:Molecule type: DNA
A:Residues: 169-172, 'T', 174-177 <TRA2>
A:Experimental source: antigen MAGE-41
R:Diing, M.; Beck, R.J.; Keller, C.J.; Penton, R.G.
  Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A:Title: Cloning and analysis of MAGE-1-related genes.
A:Reference number: JG2358; MUID:94311935; PMID:8037761
A:Accession: JG2359
A:Molecule type: mRNA
A:Residues: 1-172, 'T', 174-306, 'Q', 308-317 <DTN>
A:Cross-references: EMBL:U03040; NID:G499123; PIDN:AAA19007.1; PID:G499124
A:Experimental source: melanoma cell line DM150
C:Genetics:
A:Gene: GDB:MAGEA4; MAGE4; MAGE-X2
A:Cross-references: GDB:331119
A:Map position: Xq28-Xq28
A:introns: #status absent
C:Superfamily: tumor associated protein MAGE
F:165-177/Region: HLA-A1 binding #status predicted

Query Match      67.5%; Score 52; DB 2; Length 317;
Best Local Similarity 64.3%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TSYVKVLHHVVKTS 14
DB 282 TSYVKLHHVVRVA 295

```

RESULT 6
 S54533
 ribosomal protein L5 precursor, mitochondrial - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: protein YD8419.04; protein YD8237W; ribosomal protein Yml7
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 12-Jun-2003
 C:Accession: S54533; S17258
 R:Oliver, K.; Harris, D.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54530
 A:Accession: S54533
 A:Molecule type: DNA
 A:Residues: 1-292 <OLI>
 A:Cross-references: EMBL:Z49701; NID:8817819; PINN:CA89723.1; PID:ig817823; MIPS:YD8237W
 A:Experimental source: Strain AB972
 R:Grotmann, U.; Grack, H.R.; Kruf, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
 FEBS Lett. 284, 51-56, 1991
 A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from
 A:Reference number: S17255; MUID:91285106; PMID:2060626
 A:Accession: S17258
 A:Molecule type: protein
 A:Residues: 20-32, 'N', 24-32, 'W', 34-37, 'XX', 40, 'X', 42-44 <GRO>

A:Experimental source: strain 07173
C:Genetics:
A:Gene: SGD:MRPL7, MRPL7
A:Cross-references: SGD:S0002645
A:Map position: 4R
A:Genome: nuclear
A:Note: YDR237w
C:Superfamily: ribosomal protein L5/L11
C:Keywords: mitochondrion, protein biosynthesis, ribosome
F:1-19/Domain: transit peptide (mitochondrion) #status experimental <TNP>
F:20-292/Product: ribosomal protein L5 #status experimental <MAT>

	Query Match	54.5%	Score 42;	DB 2;	Length 293;
	Best Local Similarity	66.7%	Pred. No. 9.6;		
	Matches	8;	Conservative	2;	Mismatches
				2;	Indels
					Gaps
OY	2 SYKRVLHNNKI	13			
Db	. 24 SLVSRVHHNLVKI	35			

```

RESULT 7
T16067
hypothetical protein F13H8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C:Accession: T16067
R: Ding, H.
submitted to the EMBL Data Library, July 1995
A: Description: The sequence of C. elegans cosmid F13H8.
A: Reference number: Z18455
A: Accession: T16067
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-301 <DIN>
A: Cross-references: EMBL:U23139, NID:g722370, P1D:g722376, P1DN:AA046682.1, CESP:F13H8.6
A: Experimental source: strain Bristol N2
C: Geneticals:
A: Gene: CESP:F13H8.6
A: Introns: 61/2; 82/3; 158/3; 197/3; 240/2
C: Superfamily: Caenorhabditis elegans hypothetical protein F13H8.6

Query Match          54.5%; Score 42; DB 2; Length 301;
Best Local Similarity 54.5%; Pred. No. 9.9;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 KVLHHNVKISG 15
      |||::||:|
Db      248 KALHHLMKLTG 258

```

RESULT 8
 A96642
 hypothetical protein T13M1.1 [imported] - Arabidopsis thaliana
 C1Species: Arabidopsis thaliana (mouse-ear cress)
 C1Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C1Accession: A96642
 R1Thelodopsis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000
 A1Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A1Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yi, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A1Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A1Reference number: A66141; MUID:21016719; PMID:11130712
 A1Accession: A96642
 A1Status: preliminary
 A1Molecule type: DNA
 A1Retidues: 1-304 <STO>
 A1Cross-references: GRI:AE005173; NID:ig4508068; PIDN:MAD21412.1; GSPDB:GN00141

C:Genetics:
A:Gene: T13M11.1
A:Map position: 1

Query Match

Best Local Similarity 54.5%; Score 42; DB 2; Length 304;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 YVKVLIHHMVKISG 15
Db 244 YIKFLHDQVTISG 256

RESULT 9

D70357

conserved hypothetical protein aq_648 - Aquifex aeolicus
C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Sep-1999
C:Accession: D70357

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: D70357

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-371 <AQF>

A:Cross-references: GB:AE000700; NID:92983248; PIDN:AAC06853.1; PID:92983258; GB:AE00065
A:Experimental source: strain VFS

C:Genetics:

A:Gene: aq_648

C:Superfamily: hypothetical protein AF0390

Query Match

Best Local Similarity 54.5%; Score 42; DB 2; Length 371;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHHMWKISG 15
Db 157 IHHMAKISG 165

RESULT 10

H71631

guanine tRNA-ribosyltransferase (tgt) RP721 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C:Accession: H71631

R:Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Sichevitz-Ponten, T.; Alsmark, T.
Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71631

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-361 <AND>

A:Cross-references: GB:UJ25273; GB:UJ25269; NID:93861237; PIDN:CA15152.1; PID:9386125
A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: tgt; RP721

C:Superfamily: guanine tRNA-ribosyltransferase

Query Match 51.3%; Score 39.5; DB 2; Length 361;
Best Local Similarity 57.1%; Pred. No. 33;

Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 TSYVVKV-LHHMWKI 13
Db 310 TNYTKAVLHHWVRI 323

RESULT 11

H83659

serine/threonine-protein kinase BH0080 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H83659

R:Yakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H83659

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <STO>

A:Cross-references: GB:AP001507; GB:BA000004; NID:910172612; PIDN:BA803799.1; GSPDB:GNOC
A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0080

Query Match

Best Local Similarity 50.6%; Score 39; DB 2; Length 327;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 TSYVVKVLIHHMWKISG 15
Db 65 TSEVNVLRHFKVQCG 79

RESULT 12

A26125

heat shock protein 90 homolog - Trypanosoma cruzi
C:Species: Trypanosoma cruzi

C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Jun-1993
C:Accession: A26125

R:Dragon, E.A.; Sias, S.R.; Kato, E.A.; Gabe, J.D.
Mol. Cell. Biol. 7, 1271-1275, 1987

A:Title: The genome of Trypanosoma cruzi contains a constitutively expressed, tandemly a
A:Reference number: A26125; MUID:87172797; PMID:3350435

A:Accession: A26125

A:Molecule type: DNA

A:Residues: 1-704 <DRA>

C:Superfamily: heat shock protein 90

Query Match

Best Local Similarity 50.6%; Score 39; DB 2; Length 704;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSYVVKVLIHHMWKI 13
Db 657 TSYAERLHRMVKL 669

RESULT 13

T41978

helicase - human herpesvirus 7 (strain J1)
C:Species: human herpesvirus 7

A:Variety: strain J1
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T41978

R:Nicholas, J.
submitted to the EMBL Data Library, December 1995

A:Description: Determination and analysis of the complete nucleotide sequence of human he
A:Reference number: Z22022

A:Accession: T41978

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-820 <NIC>

A:Cross-references: EMBL:U43400; PIDN:AAC54738.1

A:Experimental source: strain J1

C:Genetics:

A:Note: U77
C:Superfamily: varicella-zoster virus gene 55 protein

Query Match

50.6%; Score 39; DB 2; Length 820;

Best Local Similarity 53.8%; Pred. No. 96;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SYKVLHMYKIS 14
| | | | |
| | | | |

Db 363 SYKVLHMYKIS 375

RESULT 14

G89453 protein F35H12.2 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001

C:Accession: G89453

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: G89453

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1142 <STO>

A:Cross-references: GB:chr_X; PIDN:AAA83178.1; PID:g1109865; GSPDB:GN00028; CESP:F35H12.

C:Genetics:

A:Gene: F35H12.2

A:Map position: X.

Query Match 50.6%; Score 39; DB 2; Length 1142;

Best Local Similarity 50.0%; Pred. No. 1.4e+02;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYKVLHMYKIS 15
| | | | |
| | | | |

Db 1101 SYKVLHMYKIS 1114

RESULT 15

S12332 ubiquitin-protein ligase (BC 6.3.2.19) - Yeast (Saccharomyces cerevisiae) (strain S288C)

N:Alternate names: protein G7168; protein YGR184C

C:Species: Saccharomyces cerevisiae

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 03-Jun-2002

C:Accession: S12332; S64502; S64498

R:Barrel, B.; Wuening, I.; Varshavsky, A.

EMBO J. 9, 3179-3189, 1990

A:Title: The recognition component of the N-end rule pathway.

A:Reference number: S12332; MUID:9106011; PMID:2209542

A:Accession: S12332

A:Molecule type: DNA

A:Residues: 1-1950 <BAR>

A:Cross-references: EMBL:X53747; NID:94743; PIDN:CAA37779.1; PID:94744

A:Experimental source: strain S288C

R:Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64499

A:Accession: S64502

A:Molecule type: DNA

A:Residues: 1-1950 <ARR>

A:Cross-references: EMBL:Z72969; NID:g1323325; PIDN:CAA97210.1; PID:g1323326; MIPS:YGR18

A:Experimental source: strain S288C

R:Hebling, U.; Hofmann, B.; Delius, H.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64498

A:Accession: S64498

A:Molecule type: DNA

A:Residues: 1615-1950 <HEB>

A:Cross-references: EMBL:Z72969; MIPS:YGR184C

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:UBR1; PTR1

A:Cross-references: SGD:S0003416; MIPS:YGR184C

A:Map position: 7R
C:Superfamily: ubiquitin-protein ligase
C:Keywords: ligase; protein degradation

Query Match 50.6%; Score 39; DB 2; Length 1950;

Best Local Similarity 58.3%; Pred. No. 2.4e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKVLHMYKIS 14
| | | | |
| | | | |

Db 1586 YKVLHMYKIS 1597

Search completed: August 17, 2004, 17:33:34
Job time: 11.1111 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 16:14:47 ; Search time 5.3333 Seconds
(without alignments)
146.447 Million cell updates/sec

Title: US-09-914-239-10
Perfect score: 77
Sequence: 1 TSVVKVLFHMVKISG.15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	314	1 MAG3_HUMAN	P43337 homo sapien
2	77	100.0	314	1 MAG3_HUMAN	P43360 homo sapien
3	71	92.2	314	1 MAG2_HUMAN	P43365 homo sapien
4	64	83.1	314	1 MAG2_HUMAN	P43366 homo sapien
5	52	67.5	317	1 MAG4_HUMAN	P43368 homo sapien
6	51	66.2	309	1 MAG1_HUMAN	P43365 homo sapien
7	46	59.7	594	1 NLFB_DROME	O9y113 drosophila
8	42	54.5	292	1 RM07_YEAST	P36519 saccharomyc
9	41	53.2	3829	1 SACS_HUMAN	O9n214 homo sapien
10	40	51.9	318	1 YZ20_AQUAE	O66411 aquifex aeo
11	39.5	51.3	361	1 TGT_RICER	O92c68 rickettsia
12	39	50.6	704	1 HS85_TRICR	P06660 trypsinosoma
13	39	50.6	820	1 HELI_HSV7J	P52357 human heipe
14	39	50.6	1950	1 UBRI_YEAST	P19812 saccharomyc
15	38	49.4	332	1 Z265_RAT	O35966 rattus norv
16	38	49.4	671	1 ANX6_CHICK	P51901 gallus gall
17	38	49.4	745	1 YU00_YEAST	P47101 saccharomyc
18	38	49.4	775	1 SM3E_HUMAN	O15041 homo sapien
19	37	48.1	305	1 M1AA_THEMA	O9w245 thermotoga
20	37	48.1	309	1 HPRK_STRSL	O9za98 streptococc
21	37	48.1	319	1 MGB2_HUMAN	O15479 homo sapien
22	37	48.1	400	1 COPB_DICDI	O23924 dictyostell
23	37	48.1	726	1 NCPB_PNACH	O9hd62 phaeochoae
24	37	48.1	775	1 SM3E_MOUSE	P70275 mus musculi
25	37	48.1	860	1 YG2D_YEAST	P53246 saccharomyc
26	37	48.1	1205	1 S122_MOUSE	P55012 mus musculi
27	37	48.1	1212	1 S122_MOUSE	P55012 mus musculi
28	36	46.8	108	1 GLB_DICDI	P56532 dictyococci
29	36	46.8	310	1 MURE_STRAP	O8cp27 staphylococ
30	36	46.8	311	1 TRIG_MOUSE	O9q317 mus musculi
31	36	46.8	315	1 SYC_HUMAN	O8ct11 staphylococ
32	36	46.8	466	1 GATB_PSEAE	O9hvt7 pseudomonas
33	36	46.8	481	1 GATB_PSEAE	O9hvt7 pseudomonas

34	36	46.8	490	1 YNC2_YEAST	P53972 saccharomyc
35	36	46.8	745	1 PURI_AQUAE	O67691 aquifex aeo
36	36	46.8	784	1 ALP4_SCHPO	O9y705 schizosacch
37	36	46.8	2222	1 DPOE_YEAST	P21951 saccharomyc
38	35.5	46.1	432	1 AMIB_HAEIN	P44493 haemophilus
39	35	45.5	119	1 YPL3_HUMAN	O9b614 homo sapien
40	35	45.5	119	1 YPL4_MOUSE	O9d013 mus musculi
41	35	45.5	124	1 YB76_PASMU	O9cdp1 pasteurella
42	35	45.5	216	1 FUCA_HAEIN	O94777 haemophilus
43	35	45.5	282	1 LPXC_CYACA	O941x3 cyanidium c
44	35	45.5	311	1 HPRK_ENTRA	O07664 enterococcu
45	35	45.5	317	1 T2RE_HUMAN	O9nyv8 homo sapien

ALIGNMENTS

RESULT 1	MAG3_HUMAN	STANDARD;	PRT;	314 AA.
ID	MAG3_HUMAN			
AC	P43357			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Melanoma-associated antigen 3 (MAGE-3 antigen) (Antigen M22-D).			
GN	MAGEA3 OR MAGE3.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND MUTAGENESIS.			
RC	TISSUE=Blood;			
RA	MEDLINE=94157413; PubMed=8113684;			
RA	Gaugier B., van den Eynde B., van der Bruggen P., Romero P.,			
RA	Gatforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.,			
RT	"Human gene MAGE-3 codes for an antigen recognized on a melanoma by			
RT	autologous cytolytic T lymphocytes."			
RL	J. Exp. Med. 179:921-930(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	MEDLINE=94311935; PubMed=8037761;			
RA	Ding M., Beck R.J., Keller C.J., Fenton R.G.;			
RT	"Cloning and analysis of MAGE-3-related genes."			
RT	Biochem. Biophys. Res. Commun. 202:549-555(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=20314869; PubMed=10854409;			
RA	Mallon A.M., Platzers M., Bates R., Gloeckner G., Borchert M.,			
RA	Nordtiek G., Striwen M.A., Kiochis P., Dangel A., Cunningham D.,			
RA	Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,			
RA	Kerry G., Greystron J.S., Clark D., Goertel M., Blechschmidt K.,			
RA	Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,			
RA	Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;			
RT	"Comparative genome sequence analysis of the Bpa/Str region in mouse			
RT	and man."			
RL	Genome Res. 10:758-775(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow, Lung, Prostate, and Skin;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scherz T.B.,			
RA	Brownstein M.J., Ustin T.B., Toehyuk S., Carninci P., Prange C.E.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			

RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16993(2002).
 CC -1- FUNCTION: Not known, though may play a role in embryonal
 CC development and tumor transformation or aspects of tumor
 CC progression. Antigen recognized on a melanoma by autologous
 CC cytolytic T lymphocytes.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
 CC LEUKEMIAS AND LYMPHOMAS.
 CC -1- SIMILARITY: Contains 1 MAGE domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U03735; AAA17446.1; -;
 DR EMBL; U82671; -; NOT ANNOTATED_CDS.
 DR EMBL; BC000340; AAH00340.1; -;
 DR EMBL; BC005963; AAH05963.1; -;
 DR EMBL; BC011744; AAH11744.1; -;
 DR EMBL; BC016803; AAH16803.1; -;
 DR EMBL; BC017389; AAH17389.1; -;
 DR PIR; JC2361; JC2361.
 DR GeneW; HGNC:6801; MAGEA3.
 DR MIM; 300174; -;
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 DR Antigen; Multigene family; Tumor antigen.
 FT DOMAIN 109 308
 FT POLY-SER.
 FT MUTAGEN 170 170 D->A: ABOLISHES HLA-A1 BINDING.
 FT MUTAGEN 176 176 Y->A: ABOLISHES HLA-A1 BINDING.
 SQ SEQUENCE 314 AA; 34747 MW; 3F5EB13D1C946A1 CRC64;
 Query Match 100.0%; Score 77; DB 1; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSYKVLHMKVKSIG 15
 DB 281 TSYKVLHMKVKSIG 295
 RESULT 2
 MAGE_HUMAN
 ID MAG6_HUMAN STANDARD; PRT; 314 AA.
 AC P43360;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Melanoma-associated antigen 6 (MAGE-6 antigen) (MAGE3B).
 GN MAGE6 OR MAGE6.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95012457; PubMed=7927540;

RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
 RA de Smet C., Brasseur F., van der Bruggen P., Lete B., Lurquin C.,
 RA Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.,
 RT "Structure, chromosomal localization, and expression of 12 genes of
 RT the MAGE family";
 RL Immunogenetics 40:360-369(1994).
 RN (2)
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RC MEDLINE=94311935; PubMed=8037761;
 RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
 RT "Cloning and analysis of MAGE-1-related genes";
 RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
 RN (3)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95369706; PubMed=7642112;
 RA Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
 RT "Sequence analysis of the MAGE gene family encoding human tumor-
 RT rejection antigens";
 RL Gene 160:287-290(1995).
 RN (4)
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=92388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantini P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR
 CC OR ASPECTS OF TUMOR PROGRESSION.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 CC FOR TESTES.
 CC -1- SIMILARITY: Contains 1 MAGE domain.
 CC -----
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 CC -----
 DR EMBL; U10691; AAA68875.1; -;
 DR EMBL; U10339; AAA19006.1; -;
 DR EMBL; D32076; BAA06842.1; -;
 DR EMBL; BC041599; AAH41599.1; -;
 DR PIR; JC2360; JC2360.
 DR GeneW; HGNC:6804; MAGEA6.
 DR MIM; 300176; -;
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 DR Antigen; Multigene family; Tumor antigen.
 FT DOMAIN 109 308
 FT POLY-SER.

SQ SEQUENCE 314 AA; 34891 MW; 29B83C7FA6E50263 CRC64;
 Query Match 100.0%; Score 77; DB 1; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMHVKTSG 15
 |||||
 DB 281 TSYVKVLHMHVKTSG 295

RESULT 3
 MAGC_HUMAN STANDARD; PRT; 314 AA.
 AC P43356; OSNSD3;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Melanoma-associated antigen 12 (MAGE-12 antigen) (MAGE12F).
 GN MAGEA12 OR MAGE12.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94102805; PubMed=8276455;
 RA de Smet C., Lurguin C., van der Bruggen P., de Plaen E., Brasseur F.,
 Boon T.;
 RT "Sequence and expression pattern of the human MAGE2 gene.";
 RL Immunogenetics 39:121-129(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=20314869; PubMed=8037761;
 RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
 RT "Cloning and analysis of MAGE-1-related genes.";
 RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20314869; PubMed=10854409;
 RA Mallon A.M., Platzner M., Bates R., Gloeckner G., Botcherby M.,
 Nordiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
 Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
 Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K.,
 Rump A., Hinzmann B., Mundy C.R., Miller W., Pousetka A., Herman G.E.,
 Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
 RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
 and man.";
 RL Genome Res. 10:758-775(2000).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heile F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udell T.B., Toohilyki S., Carninci P., Prange C.,
 Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Medan A., Rodriguez S., Sanchez A.,
 Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smillius D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR
 TRANSFORMATION OR ASPECTS OF TUMOR PROGRESSION.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 FOR TESTES.
 CC -1- SIMILARITY: Contains 1 MAGE domain.
 CC
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 CC
 CC -----
 DR EMBL; L18877; AAA19023.1; -;
 DR EMBL; U82671; -; NOT ANNOTATED_CDS.
 DR EMBL; BC003408; AAH03408.1; -;
 DR PIR; I54519; I54519.
 DR Genew; HGNC:6799; MAGEA12.
 DR MIM; 300177; -;
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 KW Antigen; Multigene family; Tumor antigen.
 FT DOMAIN 109 308 MAGE.
 FT POLY-SER.
 FT CONFLICT 40 43 C -> S (IN REF. 2).
 FT CONFLICT 187 187 D -> A (IN REF. 1).
 FT CONFLICT 300 300 S -> P (IN REF. 1).
 SQ SEQUENCE 314 AA; 34836 MW; 7E00F7CECDBF6568 CRC64;
 Query Match 92.2%; Score 71; DB 1; Length 314;
 Best Local Similarity 86.7%; Pred. No. 2.1e-05;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSYVKVLHMHVKTSG 15
 |||||
 DB 281 TSYVKVLHMHVKTSG 295

RESULT 4
 MAGE2_HUMAN STANDARD; PRT; 314 AA.
 AC P43356;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Melanoma-associated antigen 2 (MAGE-2 antigen).
 GN MAGEA2A OR MAGEA2 OR MAGE2 AND (MAGEA2B OR MAGEA2 OR MAGE2).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94102805; PubMed=8276455;
 RA de Smet C., Lurguin C., van der Bruggen P., de Plaen E., Brasseur F.,
 Boon T.;
 RT "Sequence and expression pattern of the human MAGE2 gene.";
 RL Immunogenetics 39:121-129(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20314869; PubMed=10854409;
 RA Mallon A.M., Platzner M., Bates R., Gloeckner G., Botcherby M.,
 Nordiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
 Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
 Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K.,
 Rump A., Hinzmann B., Mundy C.R., Miller W., Pousetka A., Herman G.E.,
 Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
 RT "Comparative genome sequence analysis of the Bpa/Str region in mouse

```

RT and man."
RL Genome Res. 10:758-775(2000).
RN [3]
RP MUTAGENESIS.
RC TISSUE=Blood;
RX MEDLINE=94157413; PubMed=8113684;
RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
RL autologous cytolytic T lymphocytes."
J. Exp. Med. 179:921-930(1994).
CC -1- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression. Antigen recognized on a melanoma by autologous
CC cytolytic T lymphocytes.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES.
CC -1- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC -----
DR EMBL, U18920; AAA17729.1; -
DR EMBL, U82671; -; NOT_ANNOTATED_CDS.
DR PIR, I68889; I68889; MAGEA2.
DR Genew; HGNC:6800; MAGEA2.
DR MIM: 300173; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308 MAGE.
FT DOMAIN 40 43 POLY-SER.
FT MUTAGEN 170 170 V->D: IMPROVES ABILITY TO BIND TO HLA-A1.
SQ SEQUENCE 314 AA; 35055 MW; 844F1635A2BEC7 CRC64;
Query Match 83.1%; Score 64; DB 1; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.00039;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Oy 1 TSYVKVTHHWKISG 15
Db 281 TSYVKVTHHWKISG 295
RESULT 5
MAGE4 HUMAN
ID MAGE4 HUMAN STANDARD; PRT; 317 AA.
AC PA3156;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Melanoma-associated antigen 4 (MAGE-4 antigen) (MAGE-X2) (MAGE-41).
GN MAGEA4 OR MAGE4.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95012457; PubMed=7927540;
RA de Smet C., Brasseur P., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of

```

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RT the MAGE family";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369706; PubMed=7642112;
RA Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
RL rejection antigens";
RN Gene 160:287-290(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Duodenum;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley A.C., Grimwood J.W., Green E.D., Dickinson M.C.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maizumi M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -1- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, U10687; AAA6887.1; -
DR EMBL, U10688; AAA6887.1; -
DR EMBL, U10340; AAA19007.1; -
DR EMBL, D32077; BAA06843.1; -
DR EMBL, BC017723; AAH17723.1; -
DR PIR, I38661; I38661.
DR PDB, 1IAF; 25-JUL-01.
DR Genew; HGNC:6802; MAGEA4.
DR MIM: 300175; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Polymorphism; Tumor antigen; 3D-structure.
FT DOMAIN 110 309 MAGE.
FT DOMAIN 41 43 POLY-SER.
FT VARIANT 173 173 T->A.

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FT          /FTID=VAR 004284.
FT          E -> Q (IN REF. 2).
SQ SEQUENCE 317 AA; 34929 MW; 3CFAC0EB696257C CRC64;
Query Match 67.5%; Score 52; DB 1; Length 317;
Best Local Similarity 64.3%; Pred. No. 0.06;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY          1 TSYVKVLHVMVKIS 14
DB          282 TSYVKVLEHVRYV 295

RESULT 6
MAGI_HUMAN STANDARD; PRT; 309 AA.
AC P43355; 000346;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Melanoma-associated antigen 1 (MAGE-1 antigen) (Antigen M22-E).
GN MAGE1 OR MAGE1 OR MAGE1A.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92086861; PubMed=1840703;
RA van der Bruggen P., Traversari C., Chomez P., Lurquin C., de Plaen E.,
RA van den Eynde B., Knuth A., Boon T.;
RT "A gene encoding an antigen recognized by cytolytic T lymphocytes on
RT a human melanoma."
RT Science 254:1643-1647(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RC MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes."
RT Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20314869; PubMed=10854409;
RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Borchert M.,
RA Nordiek G., Striwen M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
RA Kerry G., Greystrong J.S., Clark D., Goeldes M., Blechschmidt K.,
RA Rump A., Hinzmann B., Mundy C.R., Miller W., Pousetka A., Herman G.E.,
RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man."
RT Genome Res. 10:758-775(2000).
RN [4]
RP SEQUENCE FROM N.A. AND VARIANT ALA-32.
RX Chen H., Wang L., Mei M., Qin L., Cong X., Xu J., Wei L., Wang Y.,
RA Chen W.;
RT "The polymorphism of MAGE-1 gene in Chinese people."
RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP MUTAGENESIS.
RC TISSUE=Blood;
RX MEDLINE=94157413; PubMed=8113684;
RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
RA Gaforio J.U., de Plaen E., Leithe B., Brasseur F., Boon T.;
RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
RT autologous cytolytic T lymphocytes."
RT J. Exp. Med. 179:921-930(1994).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE=95012905; PubMed=7927954;
RA Schultz-Thayer E., Juretic A., Dellabona P., Luscher U., Stegrist W.,
RA Harder F., Heberer M., Zuber M., Spagnoli G.C.;

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RT "MAGE-1 gene product is a cytoplasmic protein."
RL Int. J. Cancer 59:435-439(1994).
CC -1- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression. Antigen recognized on a melanoma by autologous
CC cytolytic T lymphocytes.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes. Never expressed in kidney tumors, leukemias and
CC lymphomas.
CC -1- SIMILARITY: Contains 1 MAGE domain.
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CC -----
CC EMBL: M77481; AAA03229.1; -.
CC EMBL: U82670; -; NOT_ANNOTATED_CDS.
CC EMBL: AY148486; AAN62752.1; -.
CC Genew; HGNC:6796; MAGEA1.
CC MIM; 300016; -.
CC DR GO; GO:0005886; Cytoplasm membrane; TAS.
CC DR InterPro; IPR002190; MAGE.
CC DR Pfam; PF01454; MAGE; 1.
CC DR PROSITE; PS50838; MAGE; 1.
CC KW Antigen; Multigene family; Polymorphism; Tumor antigen.
CC FT DOMAIN 102 301
CC FT DOMAIN 33 36
CC FT DOMAIN 32 32
CC FT VARIANT 72 72
CC FT VARIANT 163 163
CC FT MUTAGEN 169 169
CC FT MUTAGEN 169 169
CC SQ SEQUENCE 309 AA; 34342 MW; 544EB1F9F4E9033 CRC64;

Query Match 66.2%; Score 51; DB 1; Length 309;
Best Local Similarity 64.3%; Pred. No. 0.088;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY          1 TSYVKVLHVMVKIS 14
DB          274 TSYVKVLEHVRYV 287

RESULT 7
ID NLF8_DROME STANDARD; PRT; 594 AA.
AC O9Y113;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Negative elongation factor B homolog.
GN CG32721/CG12152.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,
 RA Abri J.F., Apayanti A., An H.-U., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boshakov S.,
 RA Bortova D., Bouch D., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Meyer A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
 RA Glodok A., Gorg F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoshin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Liakopoulos P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venner E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster.";
 RA Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196012; PubMed=10731138;
 RA Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
 RA Scapleton M., Harvey D.A.;
 RT "A Drosophila complementary DNA resource.";
 RL Science 287:2222-2224(2000).
 CC -1- FUNCTION: Potential component of the NELF complex, a complex that
 CC negatively regulates the elongation of transcription by RNA
 CC polymerase II (By similarity).
 CC -1- SUBUNIT: May belong to the NELF complex (By similarity).
 CC -1- SIMILARITY: Belongs to the NELF-B family.
 CC -----
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 CC -----
 DR EMBL: AEO03441; AAF46268.1; -
 DR EMBL: AFI45659; AAD38634.1; -
 DR FLYBase: FBgn0027553; CG32721.
 KW Transcription regulation; Repressor; Nuclear protein.
 SQ SEQUENCE 594 AA; 67934 MW; D5A87283889A97F4 CRC64;

Query Match 59.7%; Score 46; DB 1; Length 594;
 Best Local Similarity 46.7%; Pred. No. 1.4;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 TSVYKVLHMKVIG 15
 | : : : : :
 Db 324 TSAIKLHLLINNEG 338

RESULT 8
 RM07_YEAST

ID RM07 YEAST STANDARD; PRT; 292 AA.
 AC P36519;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 60S ribosomal protein L7, mitochondrial precursor (YML7).
 GN MRPL7 OR YD8419.04.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / AB972;
 RA Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 20-43.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Grack H.-R., Krut V., Choi T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RL subunit from yeast mitochondria.";
 CC FEBS Lett. 284:51-56(1991).
 CC -1- SIMILARITY: Belongs to the L5P family of ribosomal proteins.
 CC -----
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 CC -----
 DR EMBL: Z49701; CAA89723.1; -
 DR PIR: S54533; S54533.
 DR GenBank: U00729;
 DR SGD: S0002645; MRPL7.
 DR InterPro: IPR002132; Ribosomal_L5.
 DR Pfam: PF00281; Ribosomal_L5; 1.
 DR Pfam: PF00673; Ribosomal_L5_C; 1.
 DR ProDom: PD001076; Ribosomal_L5; 1.
 DR PROSITE: PS00358; RIBOSOMAL_L5; FALSE_NEG.
 KW Ribosomal protein; Mitochondrion; Transit peptide.
 FT TRANSIT 1 19
 FT CHAIN 20 292 MITOCHONDRION.
 FT COMPACT 23 23 60S RIBOSOMAL PROTEIN L7.
 FT CONFLICT 33 33 C -> N (IN REF. 2).
 FT FT V -> W (IN REF. 2).
 SQ SEQUENCE 292 AA; 33099 MW; 8724840D4C928B88 CRC64;

Query Match 54.5%; Score 42; DB 1; Length 292;
 Best Local Similarity 66.7%; Pred. No. 3.6;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 SYVKVLHMKVIG 13
 | : : : : :
 Db 24 SLVKPVHHLVKI 35

RESULT 9
 SACS HUMAN
 ID SACS_HUMAN STANDARD; PRT; 3829 AA.
 AC Q9NZ74; Q94835;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sacsin.
 GN SACS OR KIAA0730.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A., AND VARIANT ALA-2619.
 RX MEDLINE=20120709; PubMed=10655055;
 RA Engert J.C., Bernabe P., Mercier J., Dore C., Lepage P., Ge B.,
 RA Bouchard J.-P., Mathieu J., Melancon S.B., Schalling M., Lander E.S.,
 RA Morgan K., Hudson T.J., Richter A.,
 RT "ARSACS, a spastic ataxia common in northeastern Quebec, is caused by
 RT mutations in a new gene encoding an 11.5-kb ORF";
 RL Nat. Genet. 24:120-125 (2000).
 RN [2]
 RP SEQUENCE OF 2826-3829 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99087487; PubMed=9872452;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XI.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro";
 RL DNA Res. 5:277-286 (1998).
 CC -1- FUNCTION: May function in chaperone-mediated protein folding.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the central nervous
 CC system. Also found in skeletal muscle and at low levels in
 CC pancreas.
 CC -1- DISEASE: Defects in SACS are the cause of autosomal recessive
 CC spastic ataxia of Charlevoix-Saguenay (ARSACS) [MIM:270550].
 CC ARSACS is an early onset neurodegenerative disease with high
 CC prevalence in the Charlevoix-Saguenay-lac-Saint-Jean region of
 CC Quebec. It is characterized by absent sensory-nerve conduction,
 CC reduced motor-nerve velocity and hypermyelination of retinal-nerve
 CC fibers.
 CC -1- SIMILARITY: Contains 1 J domain.
 CC -1- SIMILARITY: Contains 1 HEPN domain.
 CC -----
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 CC -----
 CC EMBL; AF193556; AAF31262.1; -;
 CC EMBL; AB018273; BAA34450.1; -;
 CC GeneW; HGNC:10519; SACS.
 CC MIM; 604490; -;
 CC MIM; 270550; -;
 CC GO; GO:0006457; P:protein folding; NAS.
 CC InterPro; IPR001623; DnaJ_N;
 CC InterPro; IPR007842; HEPN-
 CC SMART; SM00271; DnaJ_1;
 CC PROSITE; PS00636; DnaJ_1; FALSE_NEG.
 CC PROSITE; PS50076; DnaJ_2; 1;
 CC PROSITE; PS50910; HEPN_1;
 CC Chaperone; Polymorphism.
 CC FT DOMAIN 3556 3643 J-DOMAIN.
 CC FT DOMAIN 3701 3817 HEPN.
 CC FT VARIANT 2619 2619 V -> A.
 CC FT VARIANT 2619 2619 V -> A.
 CC SQ SEQUENCE 3829 AA; 436972 MW; 7AE990311E1B3E91 CRC64;
 CC
 CC Query Match 53.2%; Score 41; DB 1; Length 3829;
 CC Best Local Similarity 57.1%; Pred. No. 85;
 CC Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 1 TSYVXVLAHMKIS 14
 CC DB 2609 TSLIKALHWVQTS 2622
 CC
 CC RESULT 10
 CC Y220 AQUAE STANDARD; PRT; 318 AA.
 CC ID Y220 AQUAE STANDARD; PRT; 318 AA.
 CC AC O66411;
 CC DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein AA20.
 GN AA20.
 OS Aquifex aeolicus.
 OG Plasmid ecel.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxId=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL Nature 392:353-358 (1998).
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 CC -----
 CC EMBL; AB000667; AAC07963.1; -;
 CC KW Hypothetical protein; Plasmid; Complete proteome.
 CC SQ SEQUENCE 318 AA; 37793 MW; 78D752BBBDJF3801 CRC64;
 CC
 CC Query Match 51.9%; Score 40; DB 1; Length 318;
 CC Best Local Similarity 42.9%; Pred. No. 9;
 CC Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 2 SYVXVLAHMKISG 15
 CC DB 157 SHMFPHHTKSSG 170
 CC
 CC RESULT 11
 CC TGT_RICPR STANDARD; PRT; 361 AA.
 CC ID TGT_RICPR STANDARD; PRT; 361 AA.
 CC AC 092CK6;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Queneu tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine
 CC transglycosylase) (Guanine insertion enzyme).
 CC GN TGT OR RP721.
 CC OS Rickettsia prowazekii.
 CC OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 CC OC Rickettsiaceae; Rickettsiidae; Rickettsia.
 CC OX NCBI_TaxId=782;
 CC RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Anderson S.G.E., Zomrodipour A., Anderson J.O.,
 RA Scheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.,
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria";
 RL Nature 396:133-140 (1998).
 CC -----
 CC -1- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-
 CC deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His
 CC and -Tyr). After this exchange, a cyclopentadiol moiety is
 CC attached to the 7-aminomethyl group of 7-deazaguanine, resulting
 CC in the hypermodified nucleoside queuosine (Q) (7-((4,5-cis-
 CC dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
 CC guanine.

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CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the guanine tRNA-ribosyltransferase family.
CC
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CC
CC EMBL: A0235273; CA15152.1; -.
CC
DR PIR: H71631; H71631.
DR HSSP: P28720; 1PU.
DR HAMAP: MF_00168; 1.
DR InterPro: IPR004803; CcRNA_ribo_trans.
DR Pfam: PF01702; TGT; 1.
DR TIGRPFAM: TIGR00430; CcRNA_tgt; 1.
DR TIGRPFAM: TIGR00449; tgc_general; 1.
DR Qneuosine biosynthesis; Transferase; Glycosyltransferase;
KW tRNA processing; Zinc; Complete proteome.
FT ACT_SITE 93 BY SIMILARITY.
FT ACT_SITE 267 BY SIMILARITY.
FT METAL 304 ZINC (BY SIMILARITY).
FT METAL 306 ZINC (BY SIMILARITY).
FT METAL 309 ZINC (BY SIMILARITY).
FT METAL 335 ZINC (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40785 MW; 9209A3E94C41C079 CRC64;

Query Match
Best Local Similarity 51.3%; Score 39.5; DB 1; Length 361;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 TSYKVLHHWVKI 13
Db 310 TNYTKVYLHHLVRI 323

RESULT 12
HS85_TRYCR STANDARD; PRT; 704 AA.
AC P06660.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Heat shock like 85 kDa protein.
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Peru;
RC MEDLINE=8717297; PubMed=3550435;
RA Dragon E.A., Sias S.R., Kato E.A., Gabe J.D.;
RT "The genome of Trypanosoma cruzi contains a constitutively expressed,
RT tandemly arranged multicopy gene homologous to a major heat shock
RT protein."
RL Mol. Cell. Biol. 7:1271-1275(1987).
CC -1- FUNCTION: Molecular chaperone. Has ATPase activity (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the heat shock protein 90 family.
CC
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CC
CC EMBL: M15346; AAA30202.1; -.

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DR PIR: A26125; A26125.
DR HSSP: P07900; 1YER.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR001404; Hep90.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00183; HSP90; 1.
DR PRINTS: PR00775; HEATSHOCK90.
DR SMART: SM00367; HATPase_c; 1.
DR PROSITE: PS00298; HSP90; 1.
KW Chaperone; ATP-binding; Heat shock.
SQ SEQUENCE 704 AA; 80757 MW; EC39D45576BFA67 CRC64;

Query Match
Best Local Similarity 50.6%; Score 39; DB 1; Length 704;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSYKVLHHWVKI 13
Db 657 TSYAERHHWVKI 669

RESULT 13
HELI_HSV7J STANDARD; PRT; 820 AA.
ID HELI_HSV7J
AC P52357;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable helicase.
GN U77.
OS Human herpesvirus (type 7 / strain J1) (HHV7).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=57278;
RN [1]
RP SEQUENCE FROM N.A.
RA Nicholas J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: THIS PROTEIN MAY BE AN HELICASE AND IS REQUIRED FOR
CC REPLICATION OF VIRAL DNA.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL5,
CC HSV-1 57, EBV BBLF4, HCMV UL105, AND VZV 55.
CC
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CC
CC EMBL: U43400; AAC54738.1; -.
DR PIR: T41978; T41978.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003840; Herpes_helicase.
DR Pfam: PF02689; Herpes_helicase; 1.
DR SMART: SM00382; AAA; 1.
KW DNA replication; ATP-binding; Helicase.
FT NP_BIND 90 97
SQ SEQUENCE 820 AA; 92913 MW; FC253CFC888224D3 CRC64;

Query Match
Best Local Similarity 50.6%; Score 39; DB 1; Length 820;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SYKVLHHWVKI 14
Db 363 SYKVLHQQVELT 375

RESULT 14
UBR1_YEAST STANDARD; PRT; 1950 AA.
ID UBR1_YEAST

```

AC P19812;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE N-end-recognition protein (Ubiquitin-protein ligase E3 component) (N-recognin)
 GN UBRI OR PTR1 OR YGR184C OR G7168.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / GRP88;
 RX MEDLINE=91006011; PubMed=2209542;
 RA Bartel B., Wuening I., Varshavsky A.;
 RT "The recognition component of the N-end rule pathway.";
 RL EMBO J. 9:3179-3189 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=9279231; PubMed=9133739;
 RA Arroyo J., Garcia-Donaldez M., Garcia-Saez M.I., Sanchez-Perez M., Nombela C.;
 RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm of Saccharomyces cerevisiae chromosome VII.";
 RL Yeast 13:357-363 (1997).
 RN [3]
 RP SEQUENCE OF 346-1950 FROM N.A.
 RA Hebling U., Hofmann B., Delius H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Recognition component of the N-end rule pathway. Binds to proteins bearing amino-terminal residues that are destabilizing according to the N-end rule, but does not bind to otherwise identical proteins bearing stabilizing amino-terminal residues.
 CC -1- SIMILARITY: Contains 1 UBRI-type zinc finger.
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 CC -----
 CC EMBL: X53747; CA37779.1; -;
 CC EMBL: X99074; CA67528.1; -;
 CC EMBL: 272969; CA97210.1; -;
 CC PIR: S12332; S12332.
 CC Germonline: 141496; -;
 CC SGD: S0003416; UBRI.
 CC GO: GO:0005052; C:Proteasome complex (sensu Eukarya); IPT.
 CC InterPro: IPR001841; Znf_Nrecognin.
 CC Pfam: PF02207; zf-UBRI.1.
 CC SMART: SM00184; RING.1.
 CC SMART: SM00396; Znf-UBRI.1.
 CC LIGASE, Ubl conjugation pathway.
 CC KW SEQUENCE 1950 AA; 224836 MW; 33E4CD3A031AF523 CRC64;
 CC SQ

Query Match 50.6%; Score 39; DB 1; Length 1950;
 Best Local Similarity 58.3%; Pred. No. 95;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKVLHMKIS 14
 Db 1586 FIKVLHMKIS 1597
 RESULT 15
 ID 2265 RAT
 AC 035966;
 STANDARD; PRT; 332 AA.

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Zinc finger protein 265 (Zinc finger, splicing).
 GN ZNF265 OR ZIS.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=98042249; PubMed=9374836;
 RA Karginova E.A., Pentz E.S., Kazakova I.G., Norwood V.F., Carey R.M., Gomez R.A.;
 RT "Zis: a developmentally regulated gene expressed in juxtaglomerular cells.";
 RL Am. J. Physiol. 273:F731-F738 (1997).
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -1- TISSUE SPECIFICITY: Expressed in kidney; more specifically in renal juxtaglomerular (JG) cells.
 CC -1- SIMILARITY: Contains 2 RANBP2-type zinc fingers.
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 CC -----
 CC EMBL: AF013965; AAC02295.1; -;
 CC EMBL: AF013966; AAC02296.1; -;
 CC EMBL: AF013967; AAC02297.1; -;
 CC InterPro: IPR001876; Znf_RanGDP.
 CC Pfam: PF00641; zf-RanBP.2.
 CC SMART: SM00547; Znf-RBP.2.
 CC DR PROSITE: PS01358; ZF_RANBP2_1; 2.
 CC DR PROSITE: PS50199; ZF_RANBP2_2; 2.
 CC KW Zinc-finger; Nuclear protein; Repeat.
 CC FT ZN_FING 9 40 RANBP2-TYPE 1.
 CC FT ZN_FING 65 94 RANBP2-TYPE 2.
 CC FT DOMAIN 198 262 ARG/SER-RICH.
 CC SQ SEQUENCE 332 AA; 37837 MW; 90D6C7C3DB3A658F CRC64;
 CC SQ

Query Match 49.4%; Score 38; DB 1; Length 332;
 Best Local Similarity 54.5%; Pred. No. 22;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 KVLHMKISG 15
 Db 275 KVLHMKISG 285

Search completed: August 17, 2004, 17:27:21
 Job time: 6.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 17:03:13 / Search time 29.5556 Seconds
(without alignments)
160.131 Million cell updates/sec

Title: US-09-914-239-10
Sequence: 1 TSYVKVLIHMVKISG 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	83.1	314	4	Q96E03
2	52	67.5	317	4	Q14798
3	52	67.5	318	4	Q9BUN9
4	51	66.2	316	4	Q8MWH6
5	46	59.7	594	5	Q9Y113
6	43	55.8	413	3	Q9Y7D1
7	42	54.5	208	10	Q8H5V5
8	42	54.5	278	16	Q7MHG9
9	42	54.5	278	16	Q7W998
10	42	54.5	278	16	Q7VYOS
11	42	54.5	301	5	Q19436
12	42	54.5	304	10	Q9SVX1
13	42	54.5	371	16	Q6E888
14	42	54.5	382	16	Q8EM49
15	42	54.5	899	3	Q84B29
16	41	53.2	730	3	Q8X1W0

17	40.5	52.6	248	5	Q9V3Y2	Q9V3Y2 drosophila
18	40	51.9	378	16	Q8ERR7	Q8ERR7 oceanobacill
19	40	51.9	397	5	Q8EP20	Q8EP20 drosophila
20	39	50.6	159	5	Q8MO58	Q8MO58 caenorhabdi
21	39	50.6	247	16	Q7M1Z7	Q7M1Z7 bordeletia
22	39	50.6	247	16	Q7M6W2	Q7M6W2 bordeletia
23	39	50.6	249	10	Q9ST18	Q9ST18 brassica ca
24	39	50.6	269	12	Q36007	Q36007 phocid herp
25	39	50.6	317	11	Q8VGY7	Q8VGY7 mus musculu
26	39	50.6	319	11	Q8EQC7	Q8EQC7 mus musculu
27	39	50.6	327	16	Q9KG11	Q9KG11 bacillus ha
28	39	50.6	458	10	Q8S9B8	Q8S9B8 pyrus pyrif
29	39	50.6	458	10	Q9MBD0	Q9MBD0 pyrus pyrif
30	39	50.6	458	10	Q8S9B9	Q8S9B9 pyrus pyrif
31	39	50.6	820	12	Q56295	Q56295 human herpe
32	39	50.6	1350	5	Q81159	Q81159 drosophila
33	39	50.6	1362	5	Q9VDT3	Q9VDT3 drosophila
34	39	50.6	2084	5	Q869U3	Q869U3 dictyostell
35	39	50.6	2084	5	Q869U3	Q869U3 dictyostell
36	38	49.4	103	2	Q9LBN7	Q9LBN7 haemophilus
37	38	49.4	187	10	Q9SMV1	Q9SMV1 lycopersico
38	38	49.4	140	10	Q83E20	Q83E20 coxiella bu
39	38	49.4	246	2	Q9K1A1	Q9K1A1 bacteroides
40	38	49.4	373	16	Q34625	Q34625 bacillus su
41	38	49.4	379	16	Q9K6D0	Q9K6D0 bacillus ha
42	38	49.4	399	10	Q9C711	Q9C711 arabidopsis
43	38	49.4	418	9	Q8M5V9	Q8M5V9 bacterioph
44	38	49.4	441	10	Q9W4F5	Q9W4F5 brassica na
45	38	49.4	452	16	Q8R6C3	Q8R6C3 fusobacteri
					Q9K156	Q9K156 bacillus ha

ALIGNMENTS

RESULT 1
ID Q96E03 PRELIMINARY; PRT; 314 AA.
AC Q96E03;
DT 01-DIC-2001 (TREMBlrel. 19, Created)
DT 01-DIC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to melanoma antigen, family A, 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Strauberg R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013098; AAH13098.1; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PSS0838; MAGE; 1.
SQ SEQUENCE 314 AA; 35024 MW; A94F16247D1BFC0 CRC64;

Query Match 83.1%; Score 64; DB 4; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.0032;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 TSYVKVLIHMVKISG 15
DB 281 TSYVKVLIHMVKISG 295
RESULT 2
ID Q14798 PRELIMINARY; PRT; 317 AA.
AC Q14798;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser K., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen R.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Broksstein P., Tsang G.,
 RA Agbayani A., Arcaina T.T., Baxter E., Blazek R.G., Butenhof C.,
 RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
 RA Galle R., George R.A., Harris N.L., Hoekins R.A., Evans-Holm M.,
 RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshneft M., Pacleb J.M.,
 RA Park S., Seguela A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
 RA Celinker S.E.;
 RT "Full length *Drosophila melanogaster* cDNA sequence.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003441; AAF46268.1; -;
 DR FLYBASE: FBgn0027553; BCDNA:CH10333.
 DR InterPro: IPR001395; Aldo/kef_red.
 DR PROSITE: PS00063; ALDOKE TO REDUCTASE 3; 1.
 SQ SEQUENCE 594 AA; 67934 MW; D5A87283888A97F4 CRC64;

Query Match 59.7%; Score 46; DB 5; Length 594;
 Best Local Similarity 46.7%; Pred. No. 10;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TSYVKVLHMKVKG 15
 DB 324 TSAIKILHILNNEG 338

RESULT 6
 ID 09Y7D1 PRELIMINARY; PRT; 413 AA.
 AC 09Y7D1;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Transesterase.
 GN LOVD.
 OS *Aspergillus terreus*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OC NCBI_TaxID=31178;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC20542;
 RA Kennedy J., Auelair K., Kendrew S.G., Park C., Vederas J.C.,
 RA Hutchinson C.R.;
 RT "Accessory Proteins Modulate Polyketide Synthase Activity During
 RT Lovastatin Biosynthesis.";
 RL Science 0:0-0(1999).
 DR EMBL: AF141925; MAD34555.1; -;
 DR InterPro: IPR001466; Beta_lactamase.
 DR Pfam: PF00144; beta-lactamase; 1.
 SQ SEQUENCE 413 AA; 46036 MW; 731A140B6E609A24 CRC64;

Query Match 55.8%; Score 43; DB 3; Length 413;
 Best Local Similarity 57.1%; Pred. No. 25;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 SYVKVLHMKVKG 15
 ||:||||:|

DB 278 SYMKVLSLXKRDG 291
 RESULT 7
 ID 08H5V5 PRELIMINARY; PRT; 208 AA.
 AC 08H5V5;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE OUI123_B01.29 protein.
 GN OUI123_B01.29.
 OS *Oryza sativa* (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; *Oryza*.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa japonica (GA3) genomic DNA, chromosome 7, BAC
 RT clone:OUI123_B01.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003745; BAC15832.1; -;
 SQ SEQUENCE 208 AA; 22107 MW; 085184EA9CF6DCA2 CRC64;

Query Match 54.5%; Score 42; DB 10; Length 208;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TSYVKVLHMKV 10
 DB 48 TSYIKLPHL 57

RESULT 8
 ID 07WHG9 PRELIMINARY; PRT; 278 AA.
 AC 07WHG9;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Putative membrane protein.
 GN B83238.
 OS *Bordetella bronchiseptica* (Alcaligenes bronchiseptica).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; *Bordetella*.
 OC NCBI_TaxID=518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RB50 / ATCC BAA-588;
 RX MDLLINE=22827954; PubMed=12910271;
 RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bartley S.D., Mungall K.L.,
 RA Cerdano-Parraga A.M., Temple L., James K., Harris B., Cherevach I.,
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
 RA Leather S., Mole S., Norberczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitsch E., Ruter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
 RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL: BX640446; CAE33730.1; -;
 KW Complete proteome.
 SQ SEQUENCE 278 AA; 29739 MW; 41865D146368DFA7 CRC64;

Query Match 54.5%; Score 42; DB 16; Length 278;
 Best Local Similarity 58.3%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YVAVLHHMVXIS 14
 Db 29 FAKYLLHHMVSLs 40

RESULT 9
 Q7W998 PRELIMINARY; PRT; 278 AA.

AC Q7W998; 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Putative membrane protein.
 GN Bp1870.
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 NC NCBI_TaxID=519;
 RX MEDLINE=12822 / ATCC BAA-587;
 RP STRAIN=12822 / ATCC BAA-587;
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
 RA Leathers S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitz E., Ruter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640428; CAE37171.1; -.
 KW Complete proteome.
 SQ SEQUENCE 278 AA; 29739 MW; 41865D146368DFA7 CRC64;

Query Match 54.5%; Score 42; DB 16; Length 278;
 Best Local Similarity 58.3%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YVAVLHHMVXIS 14
 Db 29 FAKYLLHHMVSLs 40

RESULT 10
 Q7VY05 PRELIMINARY; PRT; 278 AA.
 AC Q7VY05; 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Putative membrane protein.
 GN Bp125.
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 NC NCBI_TaxID=520;
 RX MEDLINE=22827954; PubMed=12910271;
 RP STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
 RA Leathers S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

RA Rabinowitz E., Ruter S., Sanders M., Saunders D., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 RT Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640414; CAE41551.1; -.
 KW Complete proteome.
 SQ SEQUENCE 278 AA; 29757 MW; F7F030AE4555593 CRC64;

Query Match 54.5%; Score 42; DB 16; Length 278;
 Best Local Similarity 58.3%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YVAVLHHMVXIS 14
 Db 29 FAKYLLHHMVSLs 40

RESULT 11
 Q19436 PRELIMINARY; PRT; 301 AA.
 AC Q19436; 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F13H8.6
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 NC NCBI_TaxID=6239;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Ding H.;
 RT "The sequence of C. elegans cosmid F13H8.";
 RL Submitted (APR-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submision.";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U23139; AAK31487.1; -.
 DR PIR; T16067; T16067.
 DR Wormpep; F13H8.6; CE02640.
 KW Hypothetical protein.
 SQ SEQUENCE 301 AA; 33850 MW; 4B3DBFC506D197A6 CRC64;

Query Match 54.5%; Score 42; DB 5; Length 301;
 Best Local Similarity 54.5%; Pred. No. 27;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 KVLHHMVXIS 15
 Db 248 KALHHMLKLTG 258

RESULT 12
 Q9SYA1 PRELIMINARY; PRT; 304 AA.
 AC Q9SYA1; 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE T13M1.1 protein.
 GN T13M1.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Columbia;
 RA Federstepel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Alcafi H., Araujo R., Hultar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Ien C., Li J., Liu S.,
 RA Luro S., Schwartz J., Shin P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Becker J., Theologis A., Davis R.W.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 TRANSCRIPTION FACTORS.
 CC EMBL: AC005882; AAD21412.1; -.
 CC PIR: A96642; A96642.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH_1.
 DR SMART: SM00353; HLH_1.
 DR PROSITE: PS50888; HLH_2; 1.
 SQ SEQUENCE 304 AA; 33393 MW; 3DE4B26B3CCFCD1E CRC64;
 Query Match 54.5%; Score 42; DB 10; Length 304;
 Best Local Similarity 61.5%; Pred. No. 27;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 3 YKVLHMKVIGS 15
 Db 244 YKFLHDKVITSG 256
 RESULT 13
 066888 PRELIMINARY; PRT; 371 AA.
 AC 066888;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Hypothetical protein AQ_648.
 GN AQ_648.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificaceae; Aquifex.
 OC NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5.
 RA MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RL "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus";
 RT Nature 392:353-358(1998).
 RL Nature 392:353-358(1998).
 DR EMBL: AE000700; AAC06853.1; -.
 DR PIR: D70357; D70357.
 DR InterPro: IPR005244; Cons_hypoth423.
 DR InterPro: IPR006638; ELP3.
 DR InterPro: IPR007197; Radical_SAM.
 DR Pfam: PF04055; Radical_SAM; 1.
 DR SMART: SM00729; ELP3; 1.
 DR TIGRPFAM: TIGR00423; TIGR00423; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 371 AA; 42451 MW; 8CB5D3F29F0DF264 CRC64;
 Query Match 54.5%; Score 42; DB 16; Length 371;
 Best Local Similarity 77.8%; Pred. No. 34;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHHMKVIGS 15
 Db 157 IHHMKVIGS 165
 RESULT 14
 08EM49 PRELIMINARY; PRT; 382 AA.
 AC 08EM49;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Acyl-CoA dehydrogenase (EC 1.3.99.3).
 GN OB3011.
 OS Oceanobacillus theyensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
 OC NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=2220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RL "Genome sequence of Oceanobacillus theyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL: AP004603; BAC14967.1; -.
 DR GO: GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006089; Acyl-CoA_dh.
 DR InterPro: IPR006090; Acyl-CoA_dh_C.
 DR InterPro: IPR006091; Acyl-CoA_dh_M.
 DR InterPro: IPR006092; Acyl-CoA_dh_N.
 DR Pfam: PF00441; Acyl-CoA_dh; 1.
 DR Pfam: PF02770; Acyl-CoA_dh_M; 1.
 DR Pfam: PF02771; Acyl-CoA_dh_N; 1.
 DR PROSITE: PS00072; ACYL_COA_DH_1; 1.
 DR PROSITE: PS00073; ACYL_COA_DH_2; 1.
 KM Oxidoreductase; Complete proteome.
 SQ SEQUENCE 382 AA; 41695 MW; F6E72A4A32E3D382 CRC64;
 Query Match 54.5%; Score 42; DB 16; Length 382;
 Best Local Similarity 50.0%; Pred. No. 35;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TSYVQLHMKVIGS 14
 Db 66 TSYVQLHMKVIGS 79
 RESULT 15
 084B29 PRELIMINARY; PRT; 899 AA.
 AC 084B29;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Putative membrane-bound ATPase.
 GN TRAE.
 OS Spiroplasma kunkelii.
 OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 OC Spiroplasmataceae; Spiroplasma.
 OC NCBI_TaxID=47834;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bai X., Fazzolari T., Hogenhout S.A.;
 RL "Localization and expression analysis of trs genes of Spiroplasma
 RT kunkelii";
 RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AY233334; AAO74891.1; -.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR InterPro: IPR003593; AAA_ATPase.

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DR SMART; SM00382; AAA; 1.
SQ SEQUENCE 899 AA; 105538 MW; A552DADCFADF3BEF CRC64;
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Query Match 54.5%; Score 42; DB 2; Length 899;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy	1	TSYVKVLHHMVKIS	14
		: : : :	
Db	641	TKYLLKLYHQFKIT	654

Search completed: August 17, 2004, 17:32:04
Job time : 31.5556 secs